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Compugen Ltd
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GenCore
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1934atcgacgtaactggaaaccg ttgtaccgaagagatgagac.... US-10-086-623-5 1934 1 ttgtaccgaagaga Sequence:

Gapext 1.0 IDENTITY NUC Gapop 10.0, Scoring table

4134886 seqs, 2624710521 Searched

residues

8269772 Total number of hits satisfying chosen parameters

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a cinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

		. 4			SUMMARIES	
Result No.	Score	Query Match	, Length	DB	ID.	Description
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	518.	ъ В	15	9	ABS63516	Abs63516 Human FCT
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ALIGNMENTS

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Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary; VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour; proliferative; activator; proliferation; differentiation; motility; growth; PDGF-D receptor; antagonist; tissue remodelling; treat; atherosclerosis; wound; metastasis; ss.
                                                                                 Human Platelet Derived Growth Factor (PDGF)-D encoding partial cDNA #2
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/product= "Human PDGF-D partial polypeptide #2"
/note= "5' truncated platelet derived growth factor"
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expressing erapeutic cells exand the Novel polynucleotides encoding a novel growth factor of a platelet-derived growth factor, useful for diagnostic applications, e.g. concerning cancer.

English 5; 111pp; Fig Claim 1;

The present sequence is the 5' truncated partial cDNA #2, encoding human platelet derived growth factor (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung lambdagt10 cDNA library. It belongs to the VEGF/PDGF family. It functions as an activator of proliferation, differentiation, growth and motility of cells, that express PDGF-D receptor. This sequence is useful for inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage for generating an activated truncated form is useful for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for inhibiting tissue remodelling during the invasion of tumour cells into normal cells. PDGF-D may be used to treat wounds, atherosclerosis, metastasis and migration of smooth muscle cells

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Gene; nervous system; platelet-derived growth factor; PDGF; psychosis vascular endothelial growth factor; VEGF; neural; stem cell; memory; progenitor cell; neurodegeneration; ischaemia; neurological trauma; neuropsychiatry; learning; Parkinson's disease; Huntington's disease; Amyotrophic Lateral Sclerosis; spinal ischaemia; ischaemic stroke; spinal cord injury; cancer-related; schizophrenia; Alzheimer's diseas depression; anxiety; phobia; stress; cognitive function; aggression; drug; alcohol; abuse; obsessive compulsive behaviour; proliferation; seasonal mood disorder; personality disorder; cerebral palsy; multi-infarct, dementia; Lewy body; age related; geriatric; growth; epilepsy; brain injury; multiple sclerosis; autism; differentiation;
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 ABQ80246 standard;
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Location/Qualifiers 176. .1288 /*tag= a /product= "PDGF-D"

WO2003024478-A1

27-MAR-2003

2002WO-IB003998 19-SEP-2002; 2001US-0323381P 2001US-0326044P 19-SEP-2001; 28-SEP-2001;

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ſц Wachs À, Schanzer 저, Plate Kuhn GH, Janson AM, 저, Delfani Zhao M;

WPI; 2003-354563/33 P-PSDB; ABB80134. WPI

Use of platelet-derived growth factor, vascular endothelial growth factor, or their modulators for modulating neural stem cell or neural progenitor cell activity, particularly for treating e.g. Alzheimer's, ischemia or stroke.

22-23; 119pp; English. Claim 97; Page

The sequences given in ABQ80243-47 encode proteins which may be used in the method of the invention for alleviating or reducing a symptom of a disease or disorder of the nervous system. The method comprises administering platelet-derived growth factor (PDGF), vascular endothelial growth factor (VEGF), a combination of PDGF and VEGF, or a PDGF or VEGF agonist, to a patient in order to modulate neural stem cell or neural reducing the symptoms of a disease or disorder of the nervous system, e.g. neurodegenerative disorders, neural stem cell disorders, neural progenitor disorders, ischaemic disorders, neurological traumas, affective disorders, ischaemic disorders, neurological traumas, affective disorders, ischaemic disorders, neurological traumas, affective disorders, ischaemic disorders, huntington's disease, disorders, and disorders, Huntington's disease, harotrophic Lateral Sclerosis, spinal ischaemia, ischaemic stroke, spinal cord injury or cancer-related brain/ spinal cord injury, schizophrenia and other psychoses, depression, bipolar depression/disorder, anxiety syndromes/disorders, aggression, drug and alcohol abuse, obsessive compulsive behaviour syndromes, seasonal mood disorder, borderline personality disorder, cerebral palsy, life style drug, multi-infarct dementia, Lewy body dementia, age related/geriatric

dementia, epilepsy and injury related to epilepsy, spinal cord injury, brain injury, trauma related brain/spinal cord tissue injury, infection and inflammation related brain/spinal cord injury, environmental toxin related brain/spinal cord injury, environmental toxin related brain/spinal cord injury, multiple sclerosis, autism, attention deficit disorders, narcolepsy or sleep disorders. The PDGF and/or VEGF, is useful in the manufacture of a medicament for alleviating or treating these diseases or disorders, accelerating growth of neural stem cells or neural progenitor cells, or inducing proliferation or differentiation of these cells SSSSSSSSS

780 840 540 859 999 720 180 420 σ 0 120 439 499 619 TATTCT |||||| TATTCT CGAGGC ||||||| CGAGGC GCGGAT ||||||| CCTAGA AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA TTCCCGAACAGCTACCCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTAT ö Length 2253 Other; Indels 0 U; 0 8; ; 0 Ŧ; DB Score 1934; Pred. No. 0; 0; Mismatches G; 598 C; 490 . 0 100.0%; 701 A; 464 Conservative Query Match Best Local Similarity Matches 1934; Conser 2253 BP; 61 721 1040 1100 320 500 620 680 740 481 860 601 920 980 380 121 440 181 560 421 800 541 661 781 Sequence H 241 301 361 g අ පු a D d 8 g 8 a g g g d d ઠે ઠ ઠે a 8 ਠੇ δ ઠે ઠે 8 δ ઠે ઠે

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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnostic also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme in the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme inked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungi and cardiovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein encoding cDNA
                                                                                                                                                                                                                              Secreted protein; immunosuppressive; antiarthritic; antirheumatic antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotenotropic; neuroprotective; antibacterial; virucide; fungicide; hopthalmalogical; gene therapy; ss.
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Shi Y, Choi
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                                                                                                                                                                                                 Human secreted protein encoding cDNA (clone Id HE8TY90)
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Human; secreted protein; autoimmune disease; blood coagulation disordeblood platelet disorder; hyperproliferative disorder; renal disorder; neurodegenerative disorder; cardiovascular disorder
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der; gene; cytostatic; neuroprotective disorder; respiratory disorder; endocrine disorder; reproductive disorde gastrointestinal disorder; infectious disease; antianaemic; cy antiarthritic; immunosuppressive; antiasthmatic; antidiabetic antiinflammatory; antipsoriatic; antiparkinsonian; neuroprote 2000US-0179065P. 2000US-0180628P. 2000US-0231968P. 2001WO-US001431. 2001US-00915582 Ø G KOMATSOULIS BAKER K P. BIRSE C E. SOPPET D R. CHOIGH. FISCELLAM. NIJ. BIRSE C E. SOPPET D R OLSEN H S. MOORE P A. DUAN D R. Σ SHI Y. S MOORE P WEI P. EBNER R. ß US2002120103-A1 RUBEN S BARASH 31-JAN-2000; 04-FEB-2000; 12-SEP-2000; 17-JAN-2001; 27-JUL-2001; sapiens 29-AUG-2002 (CHOI/) (FISC/) (NIJJ/) (RUBE/) (BARA/) (BIRS/) (SOPP/) (OLSE/) (MOOR/) (WEIP/) (SHIY/) (KOMA/ ROSE/ (DUAN) Ношо

Soppet DR; Shi Y, Choi useful New secreted polypeptides and encoding polynucleotides, us preventing, treating and diagnosing diseases e.g. anemia, diabetes, asthma, psoriasis, Parkinson's and Alzheimer's. Birse Duan SC; Baker KP, , Ebner R, Barash P, SM, Komatsoulis GA, Moore PA, Wei P M, Ni J, Ruben S WPI; 2002-608160/65 P-PSDB; ABG76593. J, Σ Rosen CA, Olsen HS, Fiscella M

Claim 1; Page 373-375; 238pp; English

a human secreted protein. The sequences are useful for diagnosing or diagnosing a susceptibility to a pathological condition in a subject comprising determining the presence or absence of a mutation in the DNA or expression of the protein. The sequences are useful for identifying a binding partner to the protein comprising contacting the protein with a cityity. The DNA and protein sequences are used for preventing, treating or ameliorating a medical condition such as an autoimmune disease (e.g. multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g. afibrinogenaemia, haemophilia), blood platelet disorders (e.g. afibrinogenaemia, haemophilia), blood platelet disorders (e.g. surforome), neurodegenerative disorders (e.g. Alzheimer's disease, syndrome), neurodegenerative disorders (e.g. renal vein thrombosis, kidney infarction), cardiovascular disorders (e.g. renal vein thrombosis, kidney infarction), cardiovascular disorders (e.g. renal vein thrombosis, cegonorics), ascular disorders (e.g. aneurysm, ischaemia), respiratory disorders (e.g. tonsilitis, laryngitis), endocrine disorders (e.g. acromegaly, thyrotoxicosis), reproductive disorders (e.g. gastroenteritis, pyloric stenosis), infectious diseases (e.g. polio, rubella) and cancer. Sequences ABSS8469-ABSS8507 represent cDNA molecules encoding human secreted proteins of the invention The invention relates to an isolated nucleic acid molecule which encodes

Other; œ ü, 0 Ę, 1156 .; Ö 196 ວີ 823 A; 4001 BP; 1218 Sequence

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Query Match 98.9%; Score 1913.6; DB 6; Length 4001; Best Local Similarity 99.4%; Pred. No. 0; 1 Matches 1923; Conservative 7; Mismatches 1; Indels 3; Gaps 1; Qy 1 TTGTACCGAAGAGACGATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60	181 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA [361 TTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCA [541 CCAGAGTCATGCARAATTTGATACAGTGGAAGATCTGCTCAAGTACTTCAATTCAATTTGATACAGTGGAAGATCTTCAATTCAATTTGATACTGGACACCCCTCGGTATCGAGGC	ACGTTGCCT ACGTTGCCT ACGTTGCCT STCCTGCAC STCCTGCCAC SCCTGGCCA	OY 901 CTAGTTGACATCCAGTTGGATCACCATGAACGATTGTATCTGCAGCTCAAGACCA 960

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                                                                                                                   Human; PRO; gene; ss; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy;
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                                                   GTCCTACAAAAGACAATGTATAAGCTGTAACAGAATTTTGAATTGTTTTTTCTTT
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                      TGCCATAATAATAAGTGCTTTAGAAATTAAATCATTGTGTT
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The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polynucleotide of the invention.
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GGAACTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAACCGTGAAAAGT
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Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human; opthalmalogical; gene therapy; ss.
                                                                                 (clone Id HGCNC48)
                                                                                 Human secreted protein encoding cDNA
                                          ВР
                                           3798
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2000US-0180628P
2000US-0231968P
           2253
                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                     2001WO-US001431
                                                                     entry)
                                            CDNA;
           2240 GACGTAACTGGAAA
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                                           standard;
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04-FEB-2000;
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used 1 molecules encoding human secreted proteins, or ameliorating a medical condition. isolated nucleic acid preventing, treating c WPI; 2001-476220/51 P-PSDB; AAB85529. to preventing,

Soppet DR; Shi Y, Choi

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Baker KP, , Ebner R, M, Barash S

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Rosen CA, Komatsoulis GA, Olsen HS, Moore PA, Wei

S, E

Ruben

Ni J,

Olsen HS, P Fiscella M,

SC;

Claim 1; Page 417-418; 482pp; English.

The invention provides novel human secreted proteins and polynucleotides cencoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnosting a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardio arrest, cerebrovascular disorders e.g. cardio arrest, cerebrovascular disorders e.g. cardio arrest, cerebrovascular disorders e.g. cardio absorders e.g. corneal infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein encoding cDNA

0 Other; n: 737 G; 1123 T; 0 ວີ 749 1189 A; 3798 BP; Sequence

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Length 3798; . . DB Score 1911.6; Pred. No. 0; 98.8%; Query Match Best Local Similarity ŧ

QY 1081 ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTAATGCCATGGCAAGTAGAAA 1140	Qy 1201 GTTATATATGCACAAACACACACACAGAAATATTCATGTCTATGTGTATATAGATCAAAT 1260	1321 TAAAATCCTTTGCCAAAATAAGGGATGGTCAAATATATGAAACATGTCTTTAGAAATTT 138	QY 1441 AAGAAAGCATCTTGTATATTAAAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAG 1500 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 1558 TTCCATGAGAAGCACTGCATACTTACCTATGTGGACTGTAATAACCTGTCTCCCAAAACCA 1617 Db 1870 TTCCATGAGAAGCACTGCATACTTACCTATGTGGACTATAATAACCTGTCTCCCAAAACCA 1929 Oy 1618 TGCCATAATAATAATAATAAGTGCTTTAGAAATTAAATCATTGTGTTTTTTATGCATTTTGCTG 1677 Db 1930 TGCCATAATAATAATAATAAGAAGTGCTTTAGAAATTAAATCATTGTGTTTTTTATGCTG 1989	OY 1678 AGGCATCCTTATTCATTTAACACCTATCTCAAAAACTTAGAAGGTTTTTTATTATTAT 1737	1798 CCCCTCCACAAAGCAAA 	OY 1918 GACGTAACTGGAAA 1931	AC ABS58475; XX DT 05-NOV-2002 (first entry) XX DE Human secreted protein encoding cDNA #7. XX
Matches 1927; Conservative 0; Mismatches 4; Indels 3; Gaps 1; QY 1 TTGTACCGAAGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 60 310 TTGTACCGAAGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA 369 QY 61 TTCCCGAACAGCTACCCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCAGGAGAAT 120 QY 61 TTCCCGAACAGCTACCCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120 Db 370 TTCCCGAACAGCTACCCCAGGAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAT 120	21 ACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATTAGAGGA 	90 TGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGA 54 41 CGATGGTGTGGACAAGGAAGTTCCTCCAAGGATAAAATCAAGAACCAAACTAATTAGAGGA 54 60 CGATGGTGTGGACAAGGAAGTTCCTCCAAGGATAAAATCAAGAACGAAC	TTGCTGGAAGATTTCCAACCCGCAGCTTCAGAGCCTGGATTCAAGATTTATTT		01 AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGCCAAG		841 GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGGGGTAGAGCTAAGACCATGGCT 900	961 CCTCGATAAGAGAATGTGCACATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGA 1020

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blood platelet disorder; hyperproliferative disorder; renal disorder; neurodegenerative disorder; cardiovascular disorder; vascular disorder; respiratory disorder; endocrine disorder; reproductive disorder; gene; gastrointestinal disorder; infectious disease; antianaemic; cytostatic; antiarthritic; immunosuppressive; antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.
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Choi Soppet DR; Shi Y, Ch CE, DR,

for cancer, useful New secreted polypeptides and encoding polynucleotides, us preventing, treating and diagnosing diseases e.g. anemia, diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.

Claim 1; Page 357-359; 238pp; English

The invention relates to an isolated nucleic acid molecule which encodes a human secreted protein. The sequences are useful for diagnosing or diagnosing a susceptibility to a pathological condition in a subject comprising determining the presence or absence of a mutation in the DNA or expression of the protein. The sequences are useful for identifying a binding partner to the protein comprising contacting the protein with a conjuding partner and determining whether the binding partner effects an activity. The DNA and protein sequences are used for preventing, treating or ameliorating a medical condition such as an autoimmune disease (e.g. multiple sclerosis, mysathenia gravis), blood coagulation disorders (e.g. afibrinogenaemia, haemophilia), blood platelet disorders (e.g. sarcoidosis, Sezary syndrome), neurodegenerative disorders (e.g. Alzheimer's disease, thrombocytopenia), vascular disorders (e.g. Alzheimer's disease, parkinson's disease), renal disorders (e.g. cardiac arrest, cornegaly, thyrotoxicosis), reproductive disorders (e.g. cardiac arrest, anorchia), gastrointestinal disorders (e.g. dastroenteritis, pyloric stenosis), infectious diseases (e.g. gastroenteritis, pyloric stenosis), infectious diseases (e.g. polio, rubella) and cancer. Sequences ABSS8507 represent cDNA molecules encoding human secreted proteins of the invention

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LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder; MSD; therapy; bone growth; cartilage differentiation; wound healing; neuron growth; bone fracture; osteoporosis; osteopenia; arthritis; sarcopenia; periodontal disease; tissue atrophy; endocrine disorder; muscle loss; immobility; bone density; ds.

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Location/Qualifiers 114. .1208

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                                                                                                                                                                                                                                                                                                                                                                                   cell; angiogen
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        The present invention relates to a vascular endothelial growth factor (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules are used as modulating agents or as targets for developing modulating agents to regulate a variety of cellular processes e.g. cell proliferation, differentiation, migration and wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid are used to treat a subject with aberrant VEGF-G protein or nucleic acid expression or activity e.g. deregulated cell growth, such as cancer, hyperptrophic bone disorders, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G gene expression is inhibited through the administratic of antisense molecules or ribozymes and by targeting the regulatory region of VEGF-G to prevent transcription of the gene in target cells
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                                                                                      GGGTGAGATAAGAGACCCTTTTCCTACCAGCAACCTTACTACTAGCCTGC7
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Early detection of soft tissue sarcoma comprises determining export a gene in a first soft tissue sample and a normal soft tissue and comparing the gene expression, also useful in treating soft 2; SEQ ID NO 5810; 210pp; English. Zlotnik A; LABS (PROT-) PROTEIN DESIGN Ginsburg WM, WPI; 2004-441208/41 Example Aziz N,

ssion sample ssue pressic le sampl tissue The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 4153 BP; 1253 A; 855 C; 854 G; 1174 T; 0 U; 17 Other;

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Best Local Similarity 98.8%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 722' 602 121 902 61 662 782 181 301 361 421 962 1142 481 1082

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1140 0 200 ŝ 0 1380 557 81 1441 561 81 ű 921 00 09 80 0 FGAAGTTGGCC SCTCAAGACCA SCAAGTAGAAA ||||||||||| SCAAGTAGAAA AGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAG GTTATATATGCACAAACACACACAGAAATATATTCATGTCTATGTGTATATAGATCAAAT TGCCATAATAATAAGTGCTTTAGAAATTAAATCATTGTGTTTTTTATGCATTTTGCTG ACCATGGC CGTTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTC CTAGTTGACATCCAGTTGGATCACCATGAACGATGCGATTGTATCTGCAG(AAGAAAGCATC 1262 721 1322 661 781 1081 1382 841 1321 901 502 961 562 1021 682 1201 1802 862 1381 1441 2102 1261 922 982 501 161 ð g තු ò ð ò ð ò ð ద õ 8 ð a 8 S S ò 셤 g 8

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GATGGTGTTCAGTGAAAGATGTGGGTAGTTGAGAACTTAAAAAGTGAACATTGAAACATC
                             CCCCTCCACAAAGCAAATCCTTTCAAGAATGGCATGGGCATTCTGTATGAACCTTTCCA
                                                                            soft tissue sarcoma; cytostatic; gene therapy; vaccine; screenin
                       GTCCTACAAAAGACAATGTATAAGCTGTAACAGAATTTTGAATTTGTTTTTCTTT
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Zlotnik

Ginsburg WM,

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WPI; 2004-441208/41

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

C; 854 G; 1174 T; 0 U; 17 Other; Sequence 4153 BP; 1253 A; 855

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Score 1896.2;
Pred. No. 0;
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version - 2004
GenCore
(c) 1993
         Copyright
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model 3 using protein search, ı OM protein

23:15:13 2004, October on: Run

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322

US-10-086-623-6 1742 Title:

....DIQLDHHERCDCICSSRPPR 1 LYRRDETIQVKGNGYVQSPR.. score: Sequence: Perfect

BLOSUM62 Gapop 10.0 table: Scoring

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residues 358729299 seds, 2002273 Searched:

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Database

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19	74	00	m	9	ADA86214	Ada86214 N	Novel hum
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21	74	00.	m	9	ADA47564	Ada47564 I	Human PRO
22	74	00	m	9	ADA67359	Ada67359 I	Human PRO
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25	74	90	m	9	ADA96874	Ada96874 I	Human PRO

cells expressing and therapeutic

n factor of diagnostic

Novel polynucleotides encoding a novel growth a platelet-derived growth factor, useful for capplications, e.g. concerning cancer.

6; 111pp; English

Claim 25; Fig

Alitalo K;

Uutela M,

Lee X,

Ponten A,

X, C,

Aase K Heldin

u,

Oestman A, Eriksson

WPI; 2000-376495/32 N-PSDB; AAD00737.

polypeptide of human known as Vascular from human foetal lung

The present sequence is an N-terminally truncated platelet derived growth factor (PDGF)-D, formally Endothelial Growth Factor (VEGF)-G. It is derived

64 6 ADA79178 64 6 ADB16519 64 6 ADB16519 64 6 ADB18635 64 6 ADB18635 64 6 ADB13058 64 6 ADB13058 64 6 ADB13058 64 6 ADB24545 64 6 ADA75032 64 6 ADA85110 64 6 ADA85110	19118	87317 Novel	1651	1611 Novel	674 Human	8635 Novel	93850 Huma	19746 Novel	13058 Huma	3241 Novel	312 Human	4545 Human	8206	da75032 Human	da8511	Nove	4 Human F	80342 Human PR	Human PR	09 Human P
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	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary; VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour; proliferative; activator; proliferation; differentiation; motility; growth; PDGF-D receptor; antagonist; tissue remodelling; treat; atherosclerosis; wound; metastasis.
                                                                         Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2
                                                                                                                                                                                                                                                                                                LTD OY
                  AAY71129 standard; peptide; 322 AA
                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING
                                                                                                                                                                                                                            98US-0107852P.
98US-0113997P.
99US-0150604P.
99US-0157108P.
                                                                                                                                                                                                            99WO-US026462
                                                        entry)
                                                       (first
                                                                                                                                                                       WO200027879-A1
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                            10-NOV-1998;
28-DEC-1998;
26-AUG-1999;
04-OCT-1999;
05-OCT-1999;
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                                                       08-SEP-2000
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RESULT
AAY7112
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lambdagt10 cDNA library. It belongs to the VEGF/PDGF family. It functions as an activator of proliferation, differentiation, growth and motility of cells, that express PDGF-D receptor. This sequence is useful for inhibiting the growth of tumours, that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage for generating an activated truncated form is useful for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for inhibiting tissue remodelling during the invasion of tumour cells into normal cells. PDGF-D may be used to treat wounds, atherosclerosis, metastasis and migration of smooth muscle cells
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322 Sequence

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                                                        LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLE
                                                                                CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPG
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 Length 322;
                     Indels
Score 1742; DB 3;
Pred. No. 4.1e-166;
; Mismatches 0;
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l Similarity 100.0%;
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ADK68120 standard; protein; (first 06-MAY-2004 ADK68120; RESULT 2 ADK68120

347 AA

entry) Novel NOVX protein #23

rotic; otropic; rder; antiarteriosclerotic antidiabetic; anorectic; cardiant; hypotensive; antiarterioscles anorectic; virucide; antibacterial; fungicide; protozoacide; noc neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipemic; gene therapy; metabolic disorder; diabetes; obesit; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disoreteoarthritis; hematopoietic disorders; inflammatory skin disorethma; dyslipidemia; neurogenesis; cell differentiation; coll proliferation; hematopoiesis; wound healing; angiogenesis; chromosome mapping; pharmacogenomic.

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STIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS

CRYDFVEVEDISET

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26 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI

CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS

WO2003085124-A2.

16-OCT-2003

2003WO-US009775 01-APR-2003;

2002US-0369065P. 01-APR-2002;

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The invention relates to novel NOVX protein and their encoding DNA's, mature forms of the proteins or sequences that are at least 95% identical to, or having one or more conservative amino acid substitutions in, the proteins. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, peferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders and polypeptides may asthma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This sequence corresponds to one of the NOVX proteins of the invention.
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sease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NOVX polypeptides and polynucleotides, useful for diagnosing or treating NOVX-associated disorders, e.s., obesity, atherosclerosis, cancer, Parkinson's diagnostis, obesity, atherosclerosis,
                                                                                                                                                                                                                                                                             Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ; Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Ger Grosse WM, Gunther E, Gusev VY, Heyes MP, Lepley DM, Li L; Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman Rastelli L, Rieger DK, Shenoy SG, Shimkets RD, Smithson G,
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Pred. No. 4.7;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 46; 323pp; English.
2002US-0370279P.
2002US-0370359P.
2002US-0372019P.
2002US-0374379P.
2002US-0380973P.
2002US-0384297P.
2002US-0384329P.
2002US-0384329P.
2002US-0403491P.
2002US-0403748P.
2002US-0403748P.
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N-PSDB; ADK68119.
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Best Local Similarity
Watches 322; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated NOVX preventing, diagnos osteoarthritis, obeasthma, or infectic
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 05-APR-2002;
08-APR-2002;
08-APR-2002;
12-APR-2002;
22-APR-2002;
30-MAY-2002;
30-MAY-2002;
17-JUN-2002;
17-JUN-2002;
13-AUG-2002;
15-AUG-2002;
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08-NOV-2000; 2000WO-US030952
10-NOV-2000; 2000WO-US030873
                                                                                           Stewart TA,
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N-PSDB; AAS21336.
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les 322; Conser
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                                                                              Gerritsen ME,
Smith V, Ste
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Matches
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rtilage;
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                  EELKLA
                                                     RAKTWA
                                                                              RAKTWA
                                                                                                                                                                                                                                                                                                    and transmembrane; PRO; mammalian; cancer; lungical; tumour necrosis factor-alpha; TNF-alpha; cancer; sion; glucose; free fatty acid; skeletal muscle; cor VIIA; gene therapy.
347
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                                                                                                                                                                                                                                                                            polypeptide sequence
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                                                                                                                     LVDIQLDHHERCDCICSSRPPR
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99WO-US028651.

99WO-US028564.

99WO-US028565.

99WO-US028565.

99WO-US030095.

99WO-US030999.

99WO-US030991.

99WO-US030991.

99WO-US030911.

99WO-US030911.

99WO-US031243.

2000WO-US000219.

2000WO-US004341.

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2000WO-US004341.

2000WO-US004341.

2000WO-US006884.

2000WO-US006884.

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2000WO-US006884.

2000WO-US005601.

2000WO-US006884.

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2000WO-US006884.

2000WO-US006884.

2000WO-US013705.

2000WO-US014941.

2000WO-US014941.

2000WO-US014941.

2000WO-US014941.

2000WO-US015264.

2000WO-US015264.
                                                                                                        SRP
                                                                                                                                                                                                                                                                                                                               n; glucose;
VIIA; gene
                                                                                                                                                                                              standard; protein;
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SWQEDLENMYLDT
                                                                                                      LVDIQLDHHERCD
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02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
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7-MAY-2000;
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AAU12172-AAU12446 represent novel human secretory and transmembrane. PRO
polypeptides. The PRO polypeptides are useful to detect other PRO
polypeptides, to link bioactive molecules to cells expressing PRO
polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample. Some
of the 275 sequences are also useful to stimulate the release of tumour
necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
differentiation of chondrocytes, the proliferation or gene expression in
pericyte cells, the release of proteoglycans from cartilage, the
proliferation of inner ear utricular supporting cells or of T-
lymphocytes, the release of a cytokine from peripheral blood monocytes
(PBMCs), or the proliferation of endothelial cells. Some of the PRO
polypeptides may modulate glucose or free fatty acid uptake by skeletal
muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
VIIA. The PRO polypeptides can be used in assays to identify molecules
involved in binding interactions. The polynucleotides encoding PRO
polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy
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                                                                                                                                                                                                     Isolated , secretory and transmembrane PRO polypeptide used to detect
other PRO polypeptides, link bioactive molecules to cells expressing
polypeptides, and detect the presence of mammalian tumors e.g. lung,
breast, prostate, cervical.
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Wood WI,
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100.0%; Pred. No. 5e-166;
tive 0; Mismatches 0;
                                                 L, Desnoyers L,
ski PJ, Gurney Watanabe CK, W
                                                 Deforge L,
A, Godowski
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                                                                          A, Godow
Tumas D,
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                                                Beresini M,
E, Goddard
(GETH ) GENENTECH INC
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Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                         LLEDPQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN
                                                                              NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA
CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS
                                                                                                                                                   SEQ ID NO:314
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2000US-0219556P.
2000US-0220664P.
2000US-0220664P.
2000US-0222695P.
2000US-0222695P.
2000US-0222695P.
2000US-0222695P.
2000US-0230978P.
2000WO-US023328.
2000WS-0242922P.
2000US-0242922P.
2000US-0242928366.
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28-JUL-2000;
02-AUG-2000;
17-AUG-2000;
24-AUG-2000;
07-SEP-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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09-MAR-2001;
14-MAR-2001;
22-MAR-2001;
05-APR-2001;
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ABB84973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analogue of platelet-derived
of the invention are useful for
ing musculoskeletal disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to LP85, an analogue of platelet-derived growth factor (PDGF) homologue. Sequences of the invention are useful for the manufacture of a medicament for treating musculoskeletal disorder (MSD) which include promoting bone growth, cartilage differentiation and function, wound healing, neuron growth, preventing cartilage degradation or neuronal degeneration. They are useful for treating bone fractures, osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease, tissue atrophy, traumatised connective tissues, grafted connective tissues and/or transplanted organs, bone or muscle loss due to malignancy, endocrine disorders and immobility. They are also used for prophylactically increasing or maintaining bone density in a mammal. The present sequence is human LP85 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                         LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder; MSD; therapy; bone growth; cartilage differentiation; wound healing; neuron growth; bone fracture; osteoporosis; osteopenia; arthritis; sarcopenia; periodontal disease; tissue atrophy; endocrine disorder; muscle loss; immobility; bone density.
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treating osteoporosis, arthritis, sarcopenia, wounds, has one or
amino acid substitutions which destroy the tripeptidyl sequence o
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Pred. No. 5e-166;
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/label= Signal peptide
13. .364
                                                                                                                                                                                                                                   ocation/Qualifiers
  364 AA
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2001US-0261071P.
2001US-0261076P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gonzalez-Dewhitt
   protein;
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/label= F
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B; AAD25489.
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AAE15820 standard;
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                                                                                                                                                                                                          Homo sapiens
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                                                        26-MAR-2002
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                             AAE15820;
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                                                                                                                                                                                                                                                                                                            ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention
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                                                                                                                                                              Paon
                                                                                                                                                                                                                                   One hundred and eighty seven nucleic acids encoding PRO polypept
useful in diagnosis and treatment of cardiovascular (e.g. myocar
infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDI
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100.0%; Pred. No. 5e-166;
ive 0; Mismatches 0;
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J, Marsters
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L, Hillan KJ, Ma
CK, Williams PM,
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2001US-00854208.
2001US-00854280.
2001US-00866028.
2001US-00866034.
2001WO-US017092.
2001WO-US017443.
2001WO-US017443.
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N-PSDB; ABL88228.
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Best Local Similarity
Matches 322; Conser
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       10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
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30-MAY-2001;
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Godowski P
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ABB95579 standard; protein; 364 AA.

ABB95579

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cancer;
disorder;
                                                        Human; angiogenesis; PRO protein; cardiovascularisation; wound;
atherosclerosis; cardiac hypertrophy; gene therapy; endothelial
cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
antiarteriosclerotic;
                                          ID NO: 314
                                         ÖES
                                         protein PRO4345
                                                                                                                                                                        2000US-0219556P.
2000US-0220664P.
2000US-022695P.
2000US-022695P.
2000US-022695P.
2000US-022695P.
2000US-022695P.
2000US-0230978P.
2000US-02000S2706.
2000US-00808689.
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                                           angiogenesis related
                          entry)
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BAKER K P.
FERRARA N.
GERBER H.
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WATANABE
WILLIAMS
WOOD W I.
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25-JUL-2000;
28-JUL-2000;
02-AUG-2000;
17-AUG-2000;
24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
24-OCT-2000;
24-OCT-2000;
24-OCT-2000;
09-NOV-2000;
25-JAN-2001;
26-PEB-2001;
26-PEB-2001;
27-JAN-2001;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
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28-FEB-2001;
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28-MAR-2001;
25-MAY-2001;
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                                                                                                                                  human
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                                                                                                                                                      cardiac
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                                                                      PRO polypept
(e.g. myocar
a mammal.
                                                                                                                               The present invention provides the protein and coding sequences PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cahypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid angina, myocardial infarctions, thrombophlebitis, lymphangitis, angiogenesis (such as breast carcinoma and liver carcinoma) and healing. The present sequence is a PRO protein of the invention
            Paoi
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  Goddard
             Pan C
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                   Ye
                                                                      encoding
                                                                                          angiogenic disorders in
                                                                      acids encoding cardiovascular
           SA,
                     Wood WI,
                                                                                                                                                                                                                                            Score 1742; DB 5;
Pred. No. 5e-166;
Mismatches 0;
 Gerritsen ME,
              Marsters
Gerber H, Gerrit
L, Hillan KJ, Ma:
CK, Williams PM,
                                                                      seven nucleic
I treatment of
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                                                                                                              Claim 11; Fig 314; 567pp; English.
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tissue typing.
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           AL,
CK,
                                                                     One hundred and eighty seuseful in diagnosis and tinfarction), endothelial
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           PJ, Gurney J
JF, Watanabe
 Ferrara N,
                                         2002-171999/22
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                                                                                                                                                                                                                                                      Similarity
                                                  N-PSDB; ABL95717
                                                                                                                                                                                                                          Sequence 364 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome bioreactor;
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Matches 322
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           Godowski
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                      Stephan
  Baker
                                          WPI;
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ABO17708
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polypeptide

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L, Desnoyers L,
ski PJ, Gurney
Watanabe CK, W
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, Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                              660pp; English.
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Tumas D,
2000WO-US023522.

2000WO-US030952.

2000WO-US030952.

2000WO-US032678.

2000WO-US032678.

2000WO-US034956.

2000WO-US034956.

2000WO-US034956.

2000WO-US034956.

2001WS-00796498.

2001US-00808689.

2001US-00808689.

2001US-00854280.

2001US-00854280.

2001US-00866028.

2001US-00866034.

2001US-00866034.

2001US-00866342.

2001US-00866034.

2001US-00866034.

2001US-00866034.

2001US-00866036.

2001US-00866036.

2001US-00866036.

2001US-00866036.

2001US-00874503.

2001US-00882736.

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2001US-00882736.

2001US-00924419.

2001US-009287736.
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ME, Goddard //
Stewart TA,
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N-PSDB; ACD23945.
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 23-AUG-2000;

08-NOV-2000;

10-NOV-2000;

20-DEC-2000;

20-DEC-2000;

28-FEB-2001;

29-MAR-2001;

14-MAR-2001;

19-MAY-2001;

10-MAY-2001;

10-MAY-2001;

25-MAY-2001;

10-MAY-2001;

11-JUN-2001;

25-MAY-2001;

26-JUN-2001;

29-JUN-2001;

29-JUN-2001;

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29-AUG-2001;

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Smith V,
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3 Gao ŝ Filvaroff E, L, Sherwood S od WI, Zhang / AL, She Wood WI,

ency New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodefisyndrome (AIDS), or cancer. The invention describes an isolated nucleic acid (1) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding cof 275 nucleotide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (1) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a cetect PRO polypeptide, modulate a bioloactive molecule to a cell expressing a cetect PRO polypeptide, modulate a bioloactive molecule to a cell expressing at the uptake of glucose or free fatty acid by cells, stimulate the telease of tumour necrosis factor (TNF)-alpha from human blood, modulate the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine comperipheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome birth defects, premature aging, acquired immunodeficiency syndrome and sent sense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and

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                                                                                LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI
                                                                                                                                                                                                                                                                                                                                                                                          Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; diabetes; bone disorder; cartilage disorder; rheumatoid arthritis; obesity; sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia, hearing loss; coagulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic.
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                                                                      LYRRDETIOVKGNGYVOSPRFPNSYPRNLLLTWRLHSQENTRIQLVF
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Mismatches 0
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97US-0056974P.
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97US-0059115P.
97US-0059117P.
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18-SEP-1997;
19-SEP-1997;
19-SEP-1997;
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17-OCT-1997;
17-OCT-1997;
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970S-00663111
970S-00633239
17-OCT - 1997; 24-OCT - 1997; 24-OCT - 1997; 24-OCT - 1997; 24-OCT - 1997; 27-OCT - 1997; 28-OCT - 1997; 28-OCT - 1997; 28-OCT - 1997; 29-OCT - 1999; 20-OCT - 1999; 20-OCT
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Query Match
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0;

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Length 364;

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LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI

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CRYDFVEVEDISETSTITRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS

120

162

180

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NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA

322

LVDIQLDHHERCDCICSSRPPR

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU80870-ABU81144 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence useful.
                                                                                                                                                                                                                                                                                                                                                          diabetes, rheumatoid in mammals, stroke,
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ki PJ, Gurney AL, Sherwood S
Watanabe CK, Wood WI, Zhang
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AL,
                                                                                                                                                                                                                                                                                                                                                         New isolated PRO polypeptide useful for treating darthritis, sports injuries, obesity, hearing loss heart attack.
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,, Godowski
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99WO-US031243.

99WO-US031274.

2000WO-US000219.

2000WO-US000376.

2000WO-US003565.

2000WO-US004341.

2000WO-US004342.

2000WO-US004114.

2000WO-US004914.

2000WO-US006014.
                                                                                                                                                                                                                                                Baker KP, Beresini M,
Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                              WPI; 2003-352836/33
N-PSDB; ACA67086.
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30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
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22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to the isolation of novel human PRO ypeptides, and the polynucleotide sequences encoding them. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l and transmembrane PRO nucleic chromosome and gene mapping, as in chromosome identification.
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A, Godowski Tumas D, Wata
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2000WO-US005004.

2000WO-US005601.

2000WO-US005841.

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2000WO-US006884.

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2000WO-US013705.

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2000WO-US013264.

2000WO-US01368.

2000WO-US014941.

2000WO-US01666034.

2000WO-US017092.

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2000WO-US017096.

2000WO-US017096.

2000WO-US01735.

2000WO-US021735.

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2000WO-US021735.

2000WO-US021736.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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N-PSDB; ACA03695.
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  24-FEB-2000;

02-MAR-2000;

02-MAR-2000;

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20-MAR-2000;

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22-MAY-2000;

23-MAY-2000;

24-AUG-2000;

28-FEB-2001;

29-MAR-2001;

29-MAR-2001;

21-MAR-2001;

21-MAR-2001;

22-MAR-2001;

23-AUG-2000;

24-AUG-2001;

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    eted and transmembrane protein;
; TNF-alpha; blood; proliferation;
; tumour; genetic disorder; cytostat
                                             AA
                                                                                                                         Human; PRO polypeptide; secreted a
tumour necrosis factor-alpha; TNF-
differentiation; chondrocyte; tumous
                                             64
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98WO-US012456.
98WO-US0114524.
98WO-US019094.
98WO-US019094.
98WO-US019094.
98WO-US019094.
98WO-US019177.
98WO-US019177.
98WO-US019111.
98WO-US022991.
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99WO-US022991.
99WO-US022991.
99WO-US0228409.
99WO-US0228409.
99WO-US028409.
99WO-US028634.
99WO-US028665.
99WO-US03099.
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                                            protein;
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                                                                                                       polypeptide
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                                            standard;
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17-SEP-1998;

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11-SEP-1999;

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12-SEP-1999;

13-SEP-1999;

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15-SEP-1999;

15-SEP-1999;

16-DEC-1999;

15-SEP-1999;

16-DEC-1999;

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12-JUN-1998;

14-JUL-1998;

16-SEP-1998;

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17-SEP-1998;

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17-SEP-1999;

18-FEB-2000;

19-MAR-1999;

19-MAR-1999;

10-MAR-1999;

11-FEB-2000;

11-PEB-2000;

12-MAR-2000;

12-MAR-2000;

13-SEP-1999;

14-MAY-1999;

15-SEP-1999;

15-SEP-1999;

16-DEC-1999;

17-MAR-2000;

18-FEB-2000;

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for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals wit genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web sit at sequata.uspto.gov/psipsDIDEntry.html
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                                                                                                                                                                                                                                                                                                                                                   PESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIR
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Pred. No. 5e-166;
; Mismatches 0;
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99WO-US01903.
99WO-US01903.
99WO-US01917.
90WO-US01917.
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2001US-00808689.
2001US-00816744.
2001US-00816744.
2001US-00854280.
2001US-00854280.
2001US-008660216.
2001US-00866028.
2001US-00866034.
2001US-00866034.
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2001US-00908827.
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09-MAR-2001;
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(GETH) GENENTECH INC.

Gao Filvaroff E, L, Sherwood S od WI, Zhang S Wood WI, Deforge L, Desnoyers L, F ,, Godowski PJ, Gurney AL, umas D, Watanabe CK, Wood A, Godow Tumas D, Gerritsen ME, Goddard Smith V, Stewart ME, Goddard Stewart TA,

WPI; 2003-148238/14 N-PSDB; ABX89233.

bone Two hundred and seventy five nucleic acids encoding PRO polypeptides useful for treating pericyte-associated tumors, diabetes and various and/or cartilage disorders, e.g. arthritis.

Claim 12; Fig 186; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PROJ132 stimulates hypertrophy of a cell expressing a PRO polypeptide. PROJ132 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PROJ136, and PROJ36, PROJ26, PROJ36,

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Sequence 364 AA;
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                                                                     FVAKPGFKIYYS
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                                  Gaps
                                                                    CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYY;
                                                                                                                                                                                                                                                                                                                                             Human; PRO; secreted protein; transmembrane protein; tumour; cytcgene therapy; tumour necrosis factor-alpha; TNF-alpha; blood; proteoglycan; cartilage; cytokine; peripheral blood mononuclear cPBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell; chondrocyte cell proliferation; chondrocyte cell differentiation; pericyte cell; inner ear utricular supporting cell; T-lymphocyte endothelial cell; A-peptide; factor VIIA.
                  0
 364;
 Length
                  Indels
Score 1742; DB 6;
Pred. No. 5e-166;
Mismatches 0;
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larity 100.0%;
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17-SEP-1998;
07-OCT-1998;
29-OCT-1998;
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2000WO-US0
20-APR-1999;

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16-DEC-1999;

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18-FEB-2000;

19-MAR-2000;

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15-MAR-2000;

16-DEC-1999;

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18-FEB-2000;

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The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO bolypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 incleotide sequences, given in the specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification of PND preptide a vector, producing a PRO polypeptide, the isolated PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide, alinking a bloactive molecule to a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human bload, (or protegolycans from adulating the uptake of glucose or FRA by skeletal muscle cells (production from peripheral bload monouclear cells (production or farlymphocyte cells, or gene expression in pericyte cells (or for T-lymphocyte cells, or fendochelial cells, inhibiting the presence of a tumour in a mammal and an olipocyte cells (or for T-lymphocyte cells, or of endochelial cells), inhibiting the presence of a tumour in a mammal and an olipomulating the presence of a tumour in a mammal and an olipomulating the presence of a tumour in a mammal and gene mapping, in plunding uses as hybridisation probes, in chr
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gene mapping,
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PRO4978, useful in molecular biology, chromosome and g
generating antisense RNA and DNA, and in gene therapy.
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'ki PJ, Gurney '
Watanabe CK, W
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Pred. No. 5e-166;
Mismatches 0;
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, Godowski
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                 2001WO-US021066.
2001WO-US021735.
2001US-00908827.
2001US-00924419.
2001US-00927796.
2001US-00931836.
2001US-00028072.
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E, Goddard
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                                                                                                                                                                                                                     Baker KP, Be.
Gerritsen ME,
22-JUN-2001;
29-JUN-2001;
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                                                                                         CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGF
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98WO-US012456.

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                                                                                                                                                                                                                                                                                                                                        standard; protein;
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bioreactor; tumour
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14-SEP-1998;
14-SEP-1998;
17-SEP-1998;
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07-OCT-1998;
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07-OCT-1999;
17-SEP-1999;
01-DEC-1999;
05-JAN-1999;
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                                                      New secreted and transmembrane nucleic acids and polypeptides, as PRO, useful for treating inflammation, organ failure, atherogeardiac injury, infertility, birth defects, premature aging, AII
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             Filvaroff
                  y AL, She
Wood WI,
            Ľ,
            Desnoyers L
PJ, Gurney
                        Watanabe CK,
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            Beresini M,
E, Goddard
(GETH ) GENENTECH INC.
                        Stewart TA,
                                     2003-331925/31
                                          N-PSDB; ACA04116
                 Gerritsen ME,
                        Smith V,
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Claim 12; Fig 186; 659pp; English

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 nucleotide sequences, encoding the corresponding PRO polypeptide comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of of chondrocyte cells, the proliferation of chondrocyte cells, the release of acytokine from proteins in pricyte cells, the release of acytokine from peripheral blood mononuclear cells, the release of acytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of adjocyte cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adjocyte cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adjocyte cells, a method for detecting the presence of a tumour in a mammal and oligination of proliferation of adjocyte cells, a method for detecting the presence of a tumour in a mammal cells, a method for detecting the presence of a tumour in a mammal oligination of proliferation of adjocyte cells, a method for detecting the presence of a tumour in a mammal cells, a method for detecting the presence of a tumour in a mammal and oligination probe derived from any of the nucleic acide and polypeptides are useful for treating infury, immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acide are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typhing. The present sequence represents a PRO protein of the invention

Sequence 364 AA;

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                                                                                                                                                  LLEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVED
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   Length 364;
                       Indels
DB 6;
Query Match
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 322; Conservative 0; Mismatches 0;
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Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation stimulator; tumour; cell differentiation inihibitor; cytokine release stimulator; tumour; lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tuncervical tumour; liver tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
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                                                                                                                                             protein
                                                                                                                                                                Human; secreted and transmembrane protein; PRO
                                                                                                                                             transmembrane
                      364
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            LVDIQLDHHERCDCICSSRPPR
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99WO-US028565.
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99WO-US030911.
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99WO-US031243.
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                                                                            protein;
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Deforge L,
A, Godowski
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003-584997/55 ; ADA45704. WPI; 20 N-PSDB;

or for modulating bio: identifying agonistweight markers. e polypeptide; polypeptide, as molecular orane the pand a ansmembr Novel secreted and transmemb activity of cell expressing antagonists of polypeptide,

English 659pp; •• 18 Fig 12; Claim

Human; PRO; secreted polypeptide; transmembrane polypeptide;

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the uptake of strelease of TWN-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonuclectide probes are useful for isolating genomic and cDNA nuclectide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynuclectide (II) encoding (I) is useful in the development and soremaining of therapeutically useful reagents RN and BNA, in the preparation of PRO polypeptide, for generating transgenic animals which in turn are useful in the development and soremaining of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissue typing. This is the amino coll and (II) are useful for tissue typing. This is the amino coll and transmentance of a novel human secreted and transmentance of a novel human secreted and transm
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ski PJ, Gurney A
Watanabe CK, Wo
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A, Godowski
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Gao S; L, Filvaroff E, y AL, Sherwood S Wood WI, Zhang Zhang

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and New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome gene mapping, in generating antisense RNA and DNA, and in gene therapy WPI; 2003-687639/65 N-PSDB; ADA76135.

Claim 12; Fig 186; 659pp; English

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are

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               creagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of of human microvascular endothelial cells, for modulating the uptake of stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides which stimulate the mammablian haemoglobin-associated disorders such as various thalasseamias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from the continuation when the continuation is also available in electronic format from the continuation when the continuation is also available in electronic format from the continuation when the continuation is also available in electronic format from the continuation when the continuation is also available in electronic format from the continuation when the continuation is also available in electronic format from the continuation when the continuation is also available in electronic format from the continuation is also available in electronic format from the continuation is also available in electronic format from the continuation is also available in electronic format from the continuation is also available in electronic format from the continuation is also available in ele
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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N-PSDB; ADA18785.
20-DEC-2000;

28-FEB-2001;

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01-MAR-2001;

14-MAR-2001;

15-MAR-2001;

10-MAY-2001;

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10-MAY-2001;

119-MAY-2001;

119-MAY-2001;
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Gao W; ß / AL, Sherwood & Wood WI, Zhang Filvaroff E, Deforge L, Desnoyers L, A, Godowski PJ, Gurney Tumas D, Watanabe CK, W

2004, 23:29:11

eating nucleic acid, useful for preparing a composition for tumors. New PRO e.g.,

Claim 12; Fig 186; 660pp; English

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for chordstate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for modulating the proliferation of or gene expression in pericyte cells, for stimulating the release of groceoglycans from cartilage, for stimulating the release of cyckines from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells and for stimulating the invention. Note the sequence represents a human PRO polypeptide of the invention. Note The sequence represents a human PRO polypeptide of the invention. Note: The sequence represents a human processed also available in electronic format from USPTO at

And the state of t	Query Match Best Local Similarity 100.0%; Pred. No. 5e-166; Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIOLVFDNOFGLEEAENDI 60		61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120		121 LLEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180		181 PESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 240	223 PESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 282	241 NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300	283 NVVFFPRCLLVQRCGGRCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 342	301 LVDIQLDHHERCDCICSSRPPR 322	343 LVDIQLDHHERCDCICSSRPPR 364
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(without alignments)
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... DIQLDHHERCDCICSSRPPR 1 LYRRDETIQVKGNGYVQSPR... US-10-086-623-6 1742 score: Sequence: Title: Perfect

322

BLOSUM62 Gapop 10.0 Scoring table:

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478139 of hits satisfying chosen parameters: Total number

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478139 segs,

Searched:

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	Description	quence 6,	Ap D	ence 37, App	ence 2, Appl	e 2, Appl	equence 37, App	equence 2, Appl	equence 5, Appl	8, Appl	equence 4, Appl	equence 53, App	equence 4, Appl	ence 56, App	equence 55, App	equence 57, App	equence 54, App	4, Appl	equence 43, App	equence 35, App	, App	equence 4, Appl	ence 1, Appl	equence 2, Appl	2, Appl	യ	, Appl	equence 33, App
SUMMARIES	ID	-09-438-04		-09-457-066-		-09-564-5	-896-904-60-	-09-808-972-	-09-823-033-	-438-046-	-09-540-2	9	-09-808-6	-09-564-595D-5	-09-564-595D-5	-09-564-5	-09-564-595D-5	0	-09-457-06	-564-59	-706-968-4	-823-	-468-6	US-09-040-220D-2	27-066-	-265-6	40-224-	US-09-564-595D-33
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96-904-60-	US-09-723-749-2	US-09-823-033-2	US-10-140-002-286	US-09-468-647-2	US-09-438-046-18	US-09-438-046-19	US-09-438-046-2	US-09-468-647-29	US-09-468-647-27	US-09-468-647-26	US-08-572-225-1	US-09-285-385C-19	US-08-872-757-2	-09-850-048A-	-09-285-38	US-09-285-385C-4	US-09-374-135-6
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                                                GENEKAL INFORMATION:
APPLICANT: BRIKSSON, Ulf
APPLICANT: LASE, Karin
APPLICANT: LEG, Xuri
APPLICANT: LEG, Xuri
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-11-10
EARLIER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-05
EARLIER FILING DATE: 1999-10-05
EARLIER FILING DATE: 1999-10-05
SACHIER FILING DATE: 1999-10-05
NUMBER OF SEO ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 1.4;
; Mismatches
          Sequence 6, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:
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Matches 322; Conser
US-09-438-046-6
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                                                                               TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
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100.0%; Pred. No. 1.7e-172;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                Sequence 186, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
                                                                                                                                     APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
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NUMBER OF SEQ ID NOS: 550
EQ ID NO 186
LENGTH: 364
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Matches 322; Conser
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Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 322; Conservative 0; Mismatches 0;
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E USING
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US-09-457-066-37
Sequence 37, Application US/09457066
Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Host, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZV.
FILE REFERENCE: 98-60
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 370
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; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GR;
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE U;
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
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Best Local Similarity 100.0%;
Matches 322; Conservative
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; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37
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red. No. 1.8e-172;
Mismatches 0;
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Patent No. 6495668

GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 370
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Best Local Similarity
Matches 322; Conser
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Pred. No. 1.8e-172;
Mismatches 0;
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US-09-706-968-37
Sequence 37, Application US/09706968
Batent No. 6528050
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVJ
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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NUMBER OF SEQ ID
SOFTWARE: FastSEG
SEQ ID NO 5
LENGTH: 370
TYPE: PRT
ORGANISM: Homo 8
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LENGTH: 370
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; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
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  RESULT 7
US-09-808-972-2
'Sequence 2, Application US/09808972
'Patent No. 6630142
'GENERAL INFORMATION:
'APPLICANT: Hart, Charles E.
'APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBRO TITLE OF INVENTION: DISORDERS
'FILE REFERENCE: 00-79
'CURRENT APPLICATION NUMBER: US/09/808,972
'CURRENT APPLICATION NUMBER: US 60/235,295
'PRIOR FILING DATE: 2000-09-26
'PRIOR FILING DATE: 2000-05-03
'PRIOR FILING DATE: 2000-05-03
'PRIOR FILING DATE: 2000-05-04
'PRIOR FILING DATE: 1999-11-10
'PRIOR FILING DATE: 1999-11-10
'PRIOR FILING DATE: 1999-11-10
'PRIOR FILING DATE: 1999-05-03
'SOFTWARE: FastSEQ for Windows Version 3.0
'SEQ ID NOS: 13
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; ORGANISM: Homo sapiens
US-09-808-972-2
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Best Local Similarity
Matches 322; Conser
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Sequence 8, Application US/09438046

Patent No. 6706687

GENERAL INFORMATION:

APPLICANT: ERIKSSON, U1f

APPLICANT: LEE, Karin

APPLICANT: PONTN, Annica

APPLICANT: UNTELA, Marko

APPLICANT: OSSTWAN, Arne

APPLICANT: HELDIN, Carl-Henrik

TITLE OF INVENTION: THEREFOR, AND USES THEREOF

FILE REFERENCE: U1f Eriksson et al 1064-44833

CURRENT APPLICATION NUMBER: US/09/438,046

CURRENT FILING DATE: 1999-11-10

EARLIER FILING DATE: 1999-11-10

EARLIER FILING DATE: 1999-12-28

EARLIER FILING DATE: 1999-12-26

EARLIER APPLICATION NUMBER: 60/13,997

EARLIER PILING DATE: 1999-10-04

EARLIER PILING DATE: 1999-10-04

EARLIER PILING DATE: 1999-10-04

EARLIER FILING DATE: 1999-10-05

NUMBER OF SEO ID NOS: 31

SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                             Score 1742; DB 4;
Pred. No. 1.8e-172;
Mismatches 0;
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Windows Version
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ORGANISM: Homo sapiens
09-438-046-8
SEQ ID NOS:
FastSEQ for
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322; Conser
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Patent No. 6630142
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
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Pred. No. 1.2e-153
; Mismatches 20
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                                                                                  US-09-564-595D-53

US-09-564-595D-53

Sequence 53, Application US/09564595D

Patent No. 6495668

GENERAL INFORMATION:

APPLICANT: Gilbert, Teresa

APPLICANT: Hart, Charles E.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVE

FILE REFERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

CURRENT FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 2000-02-04
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SOFTWARE: FastSEQ for Windows Version
EQ ID NO 53
LENGTH: 370
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Best Local Similarity 86.6%;
Matches 279; Conservative
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US-09-564-595D-53
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 Score 1742; DB 4;
Pred. No. 1.8e-172;
Mismatches 0;
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Pred. No. 1.2e-153;
23; Mismatches 20;
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E USING
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; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GF;
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE;
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER FILING DATE: 2000-02-04
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SOFTWARE: FastSEQ for Windows Version
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Best Local Similarity 86.6%;
Matches 279; Conservative
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9-540-224-4
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Matches 322
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; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR FILING DATE: 1999-11-10
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.2e-153;
23; Mismatches 20;
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 279; Conser
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LENGTH: 317
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US-09-564-595D-55

Sequence 55, Application US/09564595D

Patent No. 6495668

GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
-132;
33;
                                         Score 1403; DB 4;
Pred. No. 2.5e-137;
1; Mismatches 33;
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Pred. No. 1.3e
         fusion polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: fusion polypeptide US-09-564-595D-55
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Best Local Similarity 80.0%; Pr
Matches 256; Conservative 24;
                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                         80.5%;
Similarity 83.8%;
3; Conservative
                                                                                                                                                                                                                                                                                                                          316
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                                                                                                                                                                                                                                                                                                                         DIQLDHHERCDCIC
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DVALEHHEECDCVC
; FEATURE:
; OTHER INFORMATION:
US-09-564-595D-56
                                                                263;
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LENGTH: 316
                                       Query Match
Best Local S.
Matches 263
                                                                                                                                                                                 124
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TYPE: PF
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Search completed: October 29, 2004, 23:33:57 Job time : 40 secs

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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                           Sequence 57, Application US/09564595D

Sequence 57, Application US/09564595D

Sequence 57, Application US/09564595D

GENERAL INFORMATION:

APPLICANT: Gilbert, Teresa

APPLICANT: Hart, Charles E.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REFERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

CURRENT FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 67.4%; Pred. No. 2.5e-105; Matches 213; Conservative 26; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: fusion polypeptide 09-564-595D-57
                                                                                                                                                         316
                                                                                                                                    303 DIQLDHHERCDCICSSRPPR 322
                                                                                                                                               297
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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121 DFQPAAASV---
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US-09-564-595D-57
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LENGTH: 303
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N;Alternate names: probable metalloprotease TBL-1
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31069
R;Liu, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es
J. Neurosci. 17, 755-764, 1997
A;Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
A;Reference number: Z20965; MUID:98007484; PMID:8987797
A;Accession: T31069
A;Accession: T31069
A;Accession: T31069
A;Catus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1070 <LIU>A;Residues: 1-1070 <LIU>A;Residues: 1-1070 <LIU>A;A;Cross-references: UNIPROT:P91972; EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN: AAC47015.1; PID:910(
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    Gaps
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R; Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W. Genetics 141, 271-281, 1995
A; Title: The tolkin gene is a tolloid/BMP-1 homologue that is essential A; Reference number: $58984; MuID:96042912; PMID:856976
A; Accession: S58984
A; Molecule type: mRNA
A; Reference number: $58984; MuID:96042912; PMID:856976
A; Molecule type: mRNA
A; References: UNIPROT:Q24132; EMBL:U34777; NID:g1002985; PIDN:AAC4'
A; Mote: the authors did not translate the codon for residue 722
C; Genetics:
A; Gene: tolkin
A; Cross-references: FlyBase:FBgn0004885
C; Keywords: hydrolase; metalloproteinase; zinc
F; 529-722/Domain: astacin homology <AST>
F; 519-893/Domain: EGF homology <EGF!>
F; 1118-1153/Domain: EGF homology <EGF!>
F; 614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predict F; 615/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GYVOSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVE
                                                  10 VKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRY
                                                                                                                                                                                                                                         118 YYSLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDT
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    45;
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                                                                                                                                           70 DISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSD---DYFVAKPGFKI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 TSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
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    Indels
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  Mismatches
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---RTFH
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36;
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C; Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls repe
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                                                                                                                                   13 NGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDIS
                                                                      Gaps
                                                                       10;
                                  Length 1070;
                                                                        Indels
                                                                        99
                                   Score 149; DB 2;
Pred. No. 0.002;
                                                                                                                                                                                                                                                             133 TNWESVTSSISGVSYNSPSVTDPTLIADALDKK 165
                                                                       Mismatches
                                                                                                                                                                                                                                                                                  GGCKHICENTVG-SFHC-SCREGFILAD--DEK
                                                                        34;
                                 Query Match
Best Local Similarity 28.1%;
Matches 43; Conservative
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Search completed: October 29, 2004, 23:33:12 Job time : 42 secs

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PID:92981641; PIDN:AAC2471
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                                                                                                                                                                                                                                                                                                                   As antigen precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JH0466; JQ0948
R;Farkagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A;Title: The A5 antigen, a candidate for the neuronal recognition molecule, has A;Reference number: JH0466; MUID:91337458; PMID:190825
A;Accession: JH0466
A;Molecule type: mRNA
A;Residues: 1-927 <TAK>
A;Coss-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01260.1; PID:g222
A;Comment: This protein has motifs homologus to complement components CIr and CIs
C;Comment: This protein has motifs homology citRe, A5A
C;Comment: This protein has motifs homology citRe, A5A
C;Comment: This protein is a neuronal cell surfaced cA5A
F;22-27/Product: A5 antigen; CIr/Cls repeat homology citRe, F;22-138/Domain: CIr/Cls repeat homology citRe, F;21-138/Domain: CIr/Cls repeat homology citRe, F;21-138/Domain: CIr/Cls repeat homology citRe, F;21-138/Domain: GIr/Cls repeat homology citRe, F;24-424/Domain: Giscoidin I amino-terminal homology cDN:
F;440-584/Domain: MAM homology cMAM>
F;861-883/Domain: transmembrane #status preditced cTMM>
F;861-883/Domain: transmembrane #status
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polyprotein - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-0.
C; Accession: T30337
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
A; Reference number: 220829
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Similarity 30.6%; Pre
53; Conservative 29;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISE
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Cross-references: UNIPROT:070244; EMBL:AF022247; NID:g3834379;
Genetics:
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                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                          Indels
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_cha
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_cha
C; Accession: T08618
R; Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H
J. Biol. Chem. 273, 5235-5242, 1998
A; Title: The intrinsic factor-vitamin B12 receptor and targe
A; Reference number: Z16459; MUID:98148073; PMID:9478979
A; Accession: T08618
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-3623 < MOE>
A; Cross-references: UNIPROT:070244; EMBL:AF022247; NID:93834
C; Genetics:
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65;
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No. 2.1e-05;
smatches 115;
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Pred, No. 0.00016
9; Mismatches 6
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                                                                                               <CIR4>
/ <CIR5>
His, H
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                                      F;624-740/Domain: Clr/Cls repeat homology <
F;747-782/Domain: EGF homology <EG2>
F;787-896/Domain: Clr/Cls repeat homology <
F;900-1013/Domain: Clr/Cls repeat homology
F;221,225,231,280/Binding site: zinc (His, F;221/Active site: Glu #status predicted
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Pred.
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Similarity 29.3%;
4; Conservative 29
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ilarity 24.2%;
Conservative 45
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                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 84
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                                                                                                                                             ;591-700/Domain: C1r/C1s repeat homology <C1R3>;707-742/Domain: C1r/C1s repeat homology <C1R4>;747-856/Domain: C1r/C1s repeat homology <C1R4>;747-856/Domain: C1r/C1s repeat homology <C1R5>;860-973/Domain: C1r/C1s repeat homology <C1R5>;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644;223,272/Binding site: zinc (His, His, His, Tyr) #status predicted;214/Active site: Glu #status predicted
         duplication;
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        calcium;
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C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2 C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2 C; Accession: 149540
R; Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A; Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP A; Reference number: 149540; MUID: 94229342; PMID: 817472
A; Reference number: 149540; MUID: 94229342; PMID: 817472
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-991 cRES>
A; Cross references: UNIPROT: P98063; GB: L24755; NID: 9439606; PIDN: AAA3730 C; Genetics:
A; Gene: Bmp-1
C; Superfamily: procollagen C-endopeptidase; astacin homology; CIr/CIs re C; Keywords: hydrolase; metalloproteinase; zinc
F; 135-326/Domain: astacin homology cEG1>
F; 556-592/Domain: EGF homology cEG2>
F; 556-705/Domain: EGF homology cEG2>
F; 556-705/Domain: EGF homology cEG2>
F; 518, 222, 228, 277/Binding site: zinc (His, His, His, Tyr) #status predic F; 219/Active site: Glu #status predicted
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   ternative splicing; beta-hydroxyasparagine; bone; signal sequence #status predicted <SIG>
ct. procollagen C-endopeptidase tolloid-like splicin: astacin homology <AST>
in: Clr/Cls repeat homology <CIRI>
in: Clr/Cls repeat homology <CIRI>
in: EGF homology <EGI>
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                                                                                                                                                                                                                                                                                                                                                                    10.8%; Score 187.5; DB 1; larity 39.4%; Pred. No. 1.9e-06; Conservative 18; Mismatches 43;
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C; Keywords: alterna
F;1-22/Domain: sign
F;23-986/Product: p
F;130-321/Domain: a
F;322-431/Domain: C
F;551-587/Domain: C
F;551-700/Domain: E
F;707-742/Domain: C
F;707-742/Domain: C
F;860-973/Domain: C
F;860-973/Domain: C
F;860-973/Domain: C
F;213,217,223,363,59
F;213,217,223,272/B
F;214/Active site:
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterize
ion.
A;Reference number: Z16677; MUID:98241400; PMID:9572993
A;Accession: T09456
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A;Accession: T09456
A;Cross-references: UNIPROT:060494; EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g33
C;Genetics:
A;Map position: 10p12
C;Genetics:
A;Map position: 10p12
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Gene: FlyBase:tld
Gene: FlyBase:FlyBase:FBgn0003719
Cross-references: FlyBase:FBgn0003719
;Cross-references: FlyBase:FBgn0003719
;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology;
;Keywords: duplication; hydrolase; metalloproteinase; zinc
;Keywords: duplication; homology <AST>
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C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_cha
C;Accession: A39288
R;Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B
Cell 67, 469-481, 1991
A;Title: The Drosophila dorsal-ventral patterning gene tollo
A;Reference number: A39288; MUD:92034970; PMID:1840509
A;Accession: A39288
A;Reference number: A39288; MUD:92034970; PMID:1840509
A;Accession: A39288
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-1057 <SHI>
A;Cross-references: UNIPROT:P25723; GB:M76976; NID:g157305;
C;Genetics:
A;Gene: FlyBase:tld
A;Cross-references: FlyBase:FBgn0003719
C;Superfamily: dorsal-ventral patterning protein tolloid; as
C;Keywords: duplication; hydrolase; metalloproteinase; zinc
F;136-329/Domain: astacin homology <AST>
F;352-464/Domain: Clr/Cls repeat homology <CIR1>
F;585-620/Domain: EGF homology <EGI>
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Cross-references: UNIPROT:P25723; GB:M76976; NID:g157305;
Genetics:
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Pred. No. 1.7e-05;
1; Mismatches 120;
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C;Accession: A37278; E58788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Eewj Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUD:89072730; PMID:3201241
A;Reference number: A37278; MUD:89072730; PMID:3201241
A;Reference number: A37278; MUD:89072730; PMID:3201241
A;Residues: 1-730 <WOZ
A;Cross-references: GB:W22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
C;Genetics:
A;Genetics:

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PMID:7798260
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GB:L35279; NID:g619860; PIDN:AAC41710.1; PID:g6198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730;
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A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A; Cross-references: UNIPROT: P13497; GB: M22488; NID: g179499;
R; Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A; Title: Bone morphogenetic protein-1 and a mammalian tolloi
A; Reference number: A58788; MUID: 95096114; PMID: 7798260
A; Accession: B58788
A; Molecule type: mRNA
A; Residues: 703-986 <TAK>
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R; Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M. Science 242, 1528-1534, 1988
A; Title: Novel regulators of bone formation: molecular A; Reference number: A37278; MUID:89072730; PMID:3201241
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A; Cross-references: GDB:125203; OMIM:112264
A; Map position: 8p21-8p21
C; Function:
A; Description: catalyzes hydrolysis of the C; Superfamily: procollagen C-endopeptidase;
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A; Molecule type: mR
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C; Species: Xenopus laevis (African clawed frog)
C; Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-JuC; Accession: JC2218
R; Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A; Title: Cloning and expression of cDNA encoding Xenopus laevis bone A; Reference number: JC2218; MUID: 94085787; PMID: 8262384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 procollagen C-endopeptidase (EC 3.4.24.19) precursor, spl
N;Alternate names: bone morphogenic protein 1 (BMP1)
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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38;
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                                          Mismatches
                                        33;
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C; Superfamin: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; C; Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g; 1-22/Domain: signal sequence #status predicted <SIG>
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 1-22/Domain: signal sequence #status predicted <AST>
F; 130-321/Domain: astacin homology <AST>
F; 130-321/Domain: Clr/Cls repeat homology <CIRI>
F; 551-587/Domain: Clr/Cls repeat homology <CIRI>
F; 551-587/Domain: Clr/Cls repeat homology <CIRI>
F; 551-587/Domain: Clr/Cls repeat homology <CIRI>
F; 591-700/Domain: Clr/Cls repeat homology <CIRI>
F; 591-142, 332, 363, 599/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 163-319, 185-205, 322-348, 375-397, 435-461, 488-510, 551-563, 559-572, 574-587, 591-617, 644-6 F; 213, 217, 223, 272/Binding site: zinc (His, His, His, Tyr) #status predicted F; 214/Active site: Glu #status predicted F; 555/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                   CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS
                                                                                                        LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI
                                       NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA
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5.5e-07;
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Pred. No. 5
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spinal cord-derived growth factor-B precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7592
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to 6
A;Contents: Fetal brain
A;Reference number: JC7591; MUID:21092670; PMID:11162582
A;Contents: Fetal brain
A;Accession: JC7592
A;Molecule type: mRNA
A;Residues: 1-370 <HAM>
A;Residues: 1-370 <HAM>
A;Coss-references: UNIPROT:Q9EQT1; DDBJ:AB052170
C;Genetics:
A;Gene: scdgf-B
F;1-17/Domain: secretory signal sequence #status predicted <SIG>
F;18-370/Product: spinal cord-derived growth factor-B #status predicted
F;22-370/Region: CUB domain #status predicted
F;22-370/Region: conserved motif #status predicted
F;294-308/Region: conserved motif #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-C;Accession: JC7998
R;Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A;Title: A novel murine PDGF-D splicing variant results in signific A;Reference number: JC7998; PMID:12890490
A;Reference number: JC7998
A;Molecule type: mRNA
A;Residues: 1-370 <ZHU>
C;Comment: This protein is a potent mesenchymal cell mitogen and ch
C;Genetics:
A;Gene: pdgf-D
A;Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C;Keywords: fibrosis; PDGF-D
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Conservative 2%
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

Run on:

2004, 23:24:02 October 29,

; Search time 39 Seconds (without alignments) 794.405 Million cell upda

updates/sec

Title: Perfect score: Sequence:

322 US-10-086-623-6 1742 1 LYRRDETIQVKGNGYVQSPR.....DIQLDHHERCDCICSSRPPR

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

Searched:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

0.5

seq length: 0 seq length: 200000000 Minimum DB R Maximum DB R

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* 4 0 M 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	inal cord-der	ord-deriv	-derived	den	gen C-end	gen C-end	gen C-	gen C-	c fact	ent	act	5 antigen pre	lyprotein -	rote	lloid-BMP-1 lik	ane-type fri	e facto	al prot	ctin (EC	탪	hetical p	homolog	procollagen I C-pr	active fact	rotein	ocollagen I C-	uronate-bin	mplement subco	brain-specific CUB
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II II	Query Match Best Local Similarity 99.7%; Pred. No. 1.88-127; Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
VQ da	1 LYRRDETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDI 60
\$ A	61 CRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYS 120
QQ GD	121 LLEDFQPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 180
V d d	181 PESWQEDLENMYLDTPRYRGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLA 240
<u>ک</u> م	241 NVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMA 300
da Db	301 LVDIQLDHHERCDCICSSRPPR 322

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

; Search time 191 Seconds (without alignments) 970.003 Million cell updates/sec October 29, 2004, 23:15:59

US-10-086-623-6 1742 1 LYRRDETIQVKGNGYVQSPR.....DIQLDHHERCDCICSSRPPR Title: Perfect score:

322

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 seqs,

Searched:

1825181 Total number of hits satisfying chosen parameters:

575374646 residues

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt 02:*
1: uniprot sprot:*
2: uniprot trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Teffort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
Teffort to identify novel human secreted and transmembrane proteins: a
Bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
REMBL; AY027518; AAK20082.1; -.
REMBL; AY027518; AAK30645.1; -.
REMBL; AY359116; AAQ89474.1; -.
REMBL; AY359116; AAX8089474.1; -.
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PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A. Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived factor D) (Iris-expressed growth factor long form).
Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
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MEDLINE=21092670; PubMed=11162582;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular cloning of SCDGF-B, a novel growth factor SCDGF/PDGF-C/fallotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                   Score 1742; DB 2;
Pred. No. 3e-129;
Mismatches 0;
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Commun.
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
TISSUE=Aorta;
Liu B., Liu Y.Q., I
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LLEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN
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MEDLINE=21092670; PubMed=11162582;

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

Rolem. Biophys. Res. Commun. 280:733-737(2001).

EMBL; AB052170; BAB18920.1; -.

R PIR; JC7592; JC7592.

R PIR; JC7592; JC7592.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

GO; GO:0008151; P:cell growth and/or maintenance; IEA.

R InterPro; IPR000859; CUB.

R InterPro; IPR000072; PD_growth_factor.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Spinal-cord derived growth factor-B.
Name=rSCDGF-B;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                       ; Craniata; Vertebrata; E
; Sciurognathi; Muridae;
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SMART; SM00042; CUB; 1.

SMART; SM00141; PDGF; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS50278; PDGF 2; 1.

SEQUENCE 370 AA; 42809 MW;
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Matches 280
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MEDLINE=22103462; PubMed=12107412;

Mistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J. Mistow G., Smith D., Peterson K.;

Moufard G., Smith D., Peterson K.;

Moufard G., Smith D., Peterson K.;

Thoject: steroid-response factors and similarities with retinal pigment epithelium.";

Mol. Vision 8:185-195(2002).

EMBL; AB033832; BAB18903.1; -.

R EMBL; AR33584; AAK38840.1; -.

R EMBL; AR336376; AAK56136.1; -.

R EMBL; AV027517; AAK20081.1; -.

R EMBL; AC07591; GC:membrane; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

R GO; GO:0008083; F:growth factor activity; IEA.

R InterPro; IPR000072; PD growth factor.

R InterPro; IPR000072; PD growth factor.
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                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21231380; PubMed=11331882;
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vern
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D, A.Novel Protease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
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Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Cao H.O., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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SMART; SM00042; CUB; 1.

SMART; SM00141; PDGF; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS00430; TONB DEPENDENT REC 1; UNKNOWN 1.

PROSITE; PS00430; TONB DEPENDENT REC 1; UNKNOWN 1.

SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
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PubMed=11331881;
Bergsten E., Uutela M., Li X., Pietras K., Ostman Alitalo K., Eriksson U.;
"PDGF-D is a specific, protease-activated ligand f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1742; DB 2;
Pred. No. 3.1e-129;
; Mismatches 0;
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Nat. Cell Biol. 3:512-516(2001)
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STRAIN=C57BL/6J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Yoneda Y., Ishikawa T., Ozawa K., Kira A., Hayashizaki Y.; Rakiken integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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MEDLINE=21231380; PubMed=11331882;
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D, A Novel Protease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Platelet-derived growth factor D (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109
product:platelet-derived growth factor D).
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotat
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Fukunishi Y., Fu
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-les
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STRAIN=C57BL/6J; TISSUE=Whole body;
Adachi J., Aizawa K., Akahira S., A
Arakawa T., Bono H., Carninci P., F
PRELIMINARY;
                                                                                                                                                                                                           Mus musculus (Mouse)
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Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR335583; AAK38839.1; -.

R MGD; MGI:1919035; Pdgfd.

GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.

InterPro; IPR000072; PD_growth_factor.

R InterPro; IPR000072; PD_growth_factor.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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Pred. No. 6.1e-115;
23; Mismatches 20;
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sed growth factor (Fragment).
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Submitted (JUL-2003) to the EMBL/
EMBL; AY347260; AAQ24382.1; -.
InterPro; IPR000859; CUB.
InterPro; IPR000072; PD_growth_fa
Pfam; PF00431; CUB; 1.
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SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
NCBI_TaxID=9986;
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Submitted (JUL-2003) to the
EMBL; AY347260; AAQ24382.1;
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SMART; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
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SEQUENCE FROM N.A.

C TISSUE-Mammary tumor. Metallothionien-TGF alpha model. 10 month old
virgin mouse. Taken by biopsy.;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MALachul S.F., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Bloatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Bloatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Norlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rahaksaley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Mhiting M., I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.L., A.
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TISSUE=Mammary tumor, Metallothionien-TGF alpha model.
virgin mouse. Taken by biopsy.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
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Pred. No. 4.7e-(7; Mismatches
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L. Acad. Sci. U.S.A.
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Best Local Similarity 84.2%;
Matches 176; Conservative 1
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                                                                                                                                                                                                                                                                                                                              PRELIMINARY
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SMART; SM00042; CUB;
PROSITE; PS01180; CU
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Q91946,
Q91946,
Q1946;
Q1-0CT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Spinal cord-derived growth factor.
Name=SCDGF;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiar Gallus.
NCBI_TaxID=9031;
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           FVEDSQPEAASETNWESVTSSFSGVSYHSPSITDPTLTADALDKTVAEFDTVED
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   LLEDFOPAASETNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVED
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                                                                                                                                                                                                                                                          cords, SCDGF,
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=white leghorn; TISSUE=Spinal cord;

MEDLINE=20317014; PubMed=10858496;

Hamada T., Ui-Tei K., Miyata Y.;

"A novel gene derived from developing spinal cords, E member of the PDGF/VEGF family.";

FEBS Lett. 475:97-102(2000).

-!- SIMILARITY: Belongs to the PDGF/VEGF growth facto EMBL; AB033829; BAB03265.1; -..

HSSP; Q9UCV4; 1NZI.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

GO; GO:0008151; P:cell growth and/or maintenance; IE! InterPro; IPR000859; CUB.

InterPro; IPR000072; PD_growth_factor.
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                                      209
                                      PESWQEDLENMYLDTPRYRGRSYHDRKSK
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Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD_growth_factor;
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PROSITE; PS01180; ...
PROSITE; PS50278; PDGF_2; 1...
PROSITE; PS50278; Mitogen...
A factor; Mitogen...
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SMART; SM00141; PDGF;
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OT 01-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O1-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O1-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O2-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O2-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O3-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O3-OCT-2004 (TrEMBLrel. 28, Last annotation update)

O4-OCT-2004 (TrEMBLrel. 28, Last annotation adult male product:platelet-derived library, clone:A730023611 product:platelet-derived growth factor, C polypeptide, full insert sequence)

E polypeptide, full insert sequence)

Name=Pdgfc;

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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum, Cerebandeline=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA claingh-efficiency full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length cDNA clainine-theory full-length control clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-theory full-length clainine-
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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321 HKSLTDVPLEHHEECDCVC
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Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K. Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M. Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai JOkazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

EMBL; BC037696; AAH37696.1; -.

GO; GO:0005576; C:extracellular; IDA.

GO; GO:0005161; F:platelet-derived growth factor receptor bin..

GO; GO:0008284; P:positive regulation of cell proliferation; IDA.

GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla..

GO; GO:0007171; P:transmembrane receptor protein tyrosine kin..

InterPro; IPR000859; CUB.

InterPro; IPR000072; PD_growth_factor.
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Expression driven by an MMTV-LTR enhancer.;
Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                           MMTV-LTR/Wnt1 model
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                                                                                                                                                                                         mus musculus (mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                          update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences.";
L. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 8.6e-51
                                                                                                                            C polypeptide
                                                                           sequence up
annotation
                                                                                                                                                                                                                                                                                                                          STRAIN=CZECH II;
TISSUE=Mammary tumor metastatized to lung. I
Expression driven by an MMTV-LTR enhancer.;
MEDLINE=22388257; PubMed=12477932;
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Mismatches
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Last sequ
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                                                                                                                            Platelet-derived growth factor,
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nilarity 45.3%;
Conservative 59
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23,
25,
PRELIMINARY
                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                            (Mouse)
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144; Conser
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Proc. Natl. Acad.
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NCBI_TaxID=10090;
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STRAIN=CZECH 1
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                                                01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                   Name=Pdgfc;
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58;
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SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 38886 MW;
                                                                                                                                   MALVDIQLDHHERCDCIC
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Best Local Similarity 45.3%;
Matches 144; Conservative
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I---MPQVTETT
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I---MPQVTET<sup>†</sup>
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Q9JHV8;
01-OCT-2000
01-OCT-2000
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                                                                                                                                                     RGRAKT
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Spinal cord-derived growth factor.
Name=rScdgf;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=Wistar; TISSUE=Kidney;

X MEDLINE=21092670; PubMed=11162582;

A Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

A Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

T "Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotein.";

Biochem. Biophys. Res. Commun. 280:733-737(2001).

C -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

R BMBL; AB033830; BAB19969.1; -.

R GO; GO:0008083; F:growth factor activity; IEA.

R GO; GO:0008083; F:growth factor.

R GO; GO:0008151; P:cell growth and/or maintenance; IEA.

R GO; GO:0008151; P:cell growth and/or maintenance; IEA.

R GO; GO:0008151; P:cell growth factor.

R Ffam; PF00431; CUB; 1.

R Ffam; PF00341; PDGF; 1.

R SMART; SM00141; PDGF; 1.

R SMART; SM01041; PDGF; 1.

R PROSITE; PS50278; PDGF_2; 1.

PROSITE; PS50278; PDGF_2; 1.
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                                                                                                                                                LEDFOPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDTVED
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                             RYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDY
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322 KSLTDVALEHHEECDCVC
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                                                                 LEDFOPAAASETNWESVTSSISGVSYNSPSVTDPTLIA-DALDKKIAEFDTVEDLLKYFN
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SPSVLPPSALSLDLLNNAVTAFSTVEELIRFLE
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STRAIN=Swiss-Webster/NIH;

STRAIN=Swiss-Webster/NIH;

MEDLINE=20417814; PubMed=10960785;

MEDLINE=20417814; PubMed=10960785;

MEDLINE=20417814; PubMed=10960785;

MEDLINE=20417814; PubMed=10960785;

I The mouse Pdgfc gene: dynamic expression in embryonic tissues dur organogenesis.";

Mech. Dev. 96:209-213(2000).

Resh. AF286725; AAF91483.1; -.

MGD; MGI:1859631; Pdgfc.

RO; GO:0005736; C:extracellular; IDA.

RO; GO:0005730; P:regulation of cell proliferation; IDA.

RO; GO:00050730; P:regulation of peptidyl-tyrosine phosphoryla. ..

RO; GO:0007171; P:transmembrane receptor protein tyrosine kin. ..

InterPro; IPR000072; PD_growth_factor.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Platelet-derived growth factor C.
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Pred. No. 3.7e-50;
8; Mismatches 89;
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Q9NRA1;
01-OCT-2000
01-OCT-2000
01-OCT-2003
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Best Local S
Matches 150
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genome Res. 13:2265-2270(2003).

EMBL; AF091434; AAF00049.1; -.

EMBL; AF260738; AAK51637.1; -.

EMBL; AY358493; AAQ88857.1; -.

GO; GO:0008083; F:growth factor activity; TAS.

GO; GO:0007417; P:central nervous system development; TAS.
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O9UL22;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Secretory growth factor-like protein fallotein (Spinal cord-derigrowth factor) (Platelet-derived growth factor C) (VEGF-E).
Name=hSCDGF; Synonyms=PDGFC; ORFNames=UNQ174;
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Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dow
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Uterus;
MEDLINE=20461776; PubMed=11004490;
TBai Y.J., Lee R.K., Lin S.P., Chen Y.H.;
"Identification of a novel platelet-derived growth factor-like fallotein, in the human reproductive tract.";
Biochim. Biophys. Acta 1492:196-202(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=20317014; PubMed=10858496;
Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
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MEDLINE=22887296; PubMed=12975309;
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KSLTDVALEHHEECDCVC
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Catarrhini; Hominidae; Homo.
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H., Li H., Soriano P.,
K., Ostman A., Eriksson U.;
ligand for the PDGF alpha-
                                                                                                                                                                                                  29;
                                                                                                                                                         345;
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receptor.";

Nat. Cell Biol. 2:302-309(2000).

-!- SIMILARITY: Belongs to the PDGF/VEGF growth facto EMBL; AF244813; AAF80597.1; -.

Genew; HGNC:8801; PDGFC.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

GO; GO:0008151; P:cell growth and/or maintenance; IE?

InterPro; IPR000859; CUB.

InterPro; IPR000072; PD_growth_factor.
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Last sequence update)
Last annotation update)
                                                                                                                                                       ch 42.5%; Score 739.5; DB 2; l Similarity 47.0%; Pred. No. 4.4e-50; 150; Conservative 51; Mismatches 89;
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TISSUE=Lung;
MEDLINE=20268201; PubMed=10806482;
Li X., Ponten A., Aase K., Karlsson L.
Backstrom G., Hellstrom M., Bostrom H.
Betsholtz C., Heldin C.-H., Alitalo K.
"PDGF-C is a new protease-activated li
receptor.";
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Eukaryota; Metazoa; Chordata; Creat Mammalia; Eutheria; Primates; Cat
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InterPro; IPR000072; PD_growth_Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 39029 MW;
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Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
Growth factor; Mitogen.
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590889CEA55CC5EA CRC64;
            Query Match

42.5%; Score 739.5; DB 2;
Best Local Similarity 47.0%; Pred. No. 4.4e-50;
Matches 150; Conservative 51; Mismatches 89;
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321 HKSLTDVALEHHEECDCVC 339
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model 3 using nucleic search, ı OM nucleic

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7390.676 Million cell updates/sec 04:52:57 2004, 31, October Run on:

US-10-086-623-1934 score: Perfect so Sequence:

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1934

....atcgacgtaactggaaaccg

Gapext 1.0 IDENTITY NUC table: Scoring

824507 segs, 355394441 residues Searched:

1649014 of hits satisfying chosen parameters: Total number

Minimum Maximum

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Database

'ssued_Patents NA:*
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 /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* 40 M 4 V 0

a rinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

SUMMARIES

	Description	70	e 7, Appl	36, App	1, Appl	equence 1, Appli	36, App	1, Appl	185, Ap	3, Appl	52, App	3, Appl	6, Appl	3, Appl	1, Appl	13, App	e 13,	13, App	equence 13, Appl	e 13,	13,	13,	e 13,	13,	6, 4	9	e 42, Ap	e 34,
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	ID	US-09-438	US-09-438-046-7	US-09-457-066-36	US-09-540-224-1	US-09-564-595D-1	US-09-706-968-36	US-09-808-972-1	US-10-140-002-185	0	US-09-564-595D-52	US-09-808-972-3	-09-56	US-09-438-046-3	US-09-438-046-1	US-09-222-575-13	US-09-389-681-13	-03-630-	US-09-339-338-13	-09-433-826	US-09-604-287A-13	US-09-285-480-13	-83	US-09-590-751A-13	US-09-457-066-6	US-09-706-968-6	US-09-457-066-42	US-09-564-595D-34
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Conservative

Query Match Best Local Similarity Matches 1934; Conser

; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(966) US-09-438-046-5

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·••	TITL	E OF INVE	INTION:	PLATELET	ET-1	ERIVED GR	DNA CODING
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	CORRENT		FILING DATE	•	. ר י	*^ ' 0 C * ' C ^ /	
•	EARLIER		APPLICATION	Z	9 :		
	EARLIER	IER FILIN	JG DATE	: 1998-1	11-		
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••	EARL	IER APPLI	APPLICATION	NUMBER	9	0/150,604	
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RESULT 2
US-09-438-046-7
i Sequence 7, Application US/09438046
j Patent No. 6706687
j GENERAL INFORMATION:
j APPLICANT: ERIKSSON, Ulf
h APPLICANT: LEE, Kuri
h APPLICANT: LEE, Xuri
h APPLICANT: UUTELA, Marko
h APPLICANT: ALITALO, Kari
h APPLICANT: ALITALO, Kari
h APPLICANT: HELDIN, Carl-Henrik
h TITLE OF INVENTION: THEREFOR, AND USES THEREOF
h TITLE OF INVENTION: THEREFOR, AND USES THEREOF
h TITLE OF INVENTION UNBER: US/09/438,046
current FILING DATE: 1999-11-10
h EARLIER FILING DATE: 1998-11-10
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EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.0%;
Matches 1934; Conservative
                                                                                     NAME/KEY: CDS
LOCATION: (176)..(1288)
09-438-046-7
                                                                        ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 0;
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                                                          Sequence 36, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVI
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1882
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Best Local Similarity 99.6%;
Matches 1507; Conservative
                          ... (1338)
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (226).
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APPLICANT: Gilbert, Teresa; APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZV; FILE REFERENCE: 99-19; CURRENT APPLICATION NUMBER: US/09/564,595D; CURRENT FILING DATE: 2000-05-03
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       US-09-540-224-1
; Sequence 1, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROW
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE US:
; FILE REFERENCE: 00-28
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 0;
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Best Local Similarity 99.6%;
Matches 1507; Conservative
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LOCATION: (226)...(1338)
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; Sequence 36, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG;
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR FILING DATE: 2000-11-06
; PRIOR FILING DATE: 2000-3-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 0;
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PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.
LENGTH: 1882
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ORGANISM: Homo sapiens
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LOCATION: (226)
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                                     Score 1491.8;
Pred. No. 0;
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Best Local Similarity 99.6%;
Matches 1507; Conservative
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SEQ ID NO 36
LENGTH: 1882
TYPE: DNA
ORGANISM: HOMO 8
FEATURE:
NAME/KEY: CDS
LOCATION: (226).
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Sequence 1, Application US/09808972

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Topouzis, Stavros

APPLICANT: Topouzis, Stavros

TITLE OF INVENTION: DESCRIBERS

FILE REFERENCE: 00-79

CURRENT APPLICATION NUMBER: US/09/808,972

CURRENT APPLICATION NUMBER: US 60/235,295

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-05-03

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 3.0

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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smtrw, Victoria
APPLICANT: Smtrw, Victoria
APPLICANT: Stewart, Timothy A.
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APPLICANT: Watanabe, Colin K
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Patent No. 6725730
GENERAL INFORMATION:
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Matches 1507; Conservative
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; NAME/KEY: CDS
; LOCATION: (226).
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Sequence 3, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF;
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVI
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                               Score 795.4; DB 4;
Pred. No. 5.1e-199;
; Mismatches 226;
                                                                                                                                                                                                            0;
                                                                                                                                                                                               Query Match
Best Local Similarity 78.7%;
Matches 1007; Conservative
                                                                                                                                         ; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-540-224-3
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                           Score 1003.4; DB 4
Pred. No. 1.1e-253;
0; Mismatches 1;
                           Query Match
Best Local Similarity 99.9%;
Matches 1004; Conservative
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TYPE: DNA
ORGANISM: Homo
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US-09-564-595D-52

Sequence 52, Application US/09564595D

Patent No. 6495668

GENERAL INFORMATION:

APPLICANT: Gilbert, Teresa

APPLICANT: Hart, Charles E.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVE

FILE REFERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

CURRENT FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 4.0
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                        Score 795.4; DB 4
Pred. No. 5.1e-199
0; Mismatches 226
                        Query Match
Best Local Similarity 78.7%;
Matches 1007; Conservative
          (1205)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93).
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                                                             ATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGG
                                                                                                                                                                                                                                           APPLICANT: HAIL, CHAILES E.
APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
SOFTWARE: FABLEQ for Windows Version 3.0
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                                                                                                                                                         Sequence 3, Application US/09808972
Patent No. 6630142
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
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llarity 78.7%;
Conservative
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; LOCATION: (93)
US-09-808-972-3
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
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Best Local Simi
Matches 1007;
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WESULT 13
US-09-438-046-3
US-09-438-046-3
Sequence 3, Application US/09438046
Fatent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: LEE, Karin
APPLICANT: LEE, Karin
APPLICANT: LOUTELA, Marko
APPLICANT: LOUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UTELA, Kari
APPLICANT: UTELA, Kari
APPLICANT: UTELET-DERIVED GROWTH FACTOR D,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES
TITLE OF INVENTION THEREFOR, AND USES
TITLE OF INVENTION UNBER: 60/13/997
EARLIER FILING DATE: 1999-11-10
BARLIER APPLICATION NUMBER: 60/113,997
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-10-08
EARLIER FILING DATE: 1999-10-08
EARLIER FILING DATE: 1999-10-05
MUMBER OF SEQ ID NOS: 31
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                                                                                          US-09-564-595D-6

US-09-564-595D-6

Sequence 6, Application US/09564595D

Patent No. 6495668

GENERAL INFORMATION:

APPLICANT: Gilbert, Teresa

APPLICANT: Hart, Charles E.

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REFERENCE: 99-19

CURRENT FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: US 09/304,216

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.9%; Pred. No. 2.2e-173;
Matches 549; Conservative 259; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: degenerate sequence
NAME/KEY: misc_feature
LOCATION: (1)...(1110)
OTHER INFORMATION: n = A,T,C or G
                                          1469
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                        1451 ACTTTATTCAGTATATTTA
                GTTTTTTTGGTATATATA
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CCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC
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1.1e-83;
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ir Use
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Pred. No. 1.2e-46;
); Mismatches 12;
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Pred. No. 1.1e
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; Sequence 13, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; TITLE OF INVENTION: Compositions for the
; TITLE OF INVENTION: and Methods for Thei
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEQ for Windows Version 3.0
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER FILING DATE: 1999-10-04
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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Best Local Similarity 94.0%;
Matches 234; Conservative
                                                                                                                                                                    Query Match
Best Local Similarity 99.2%;
Matches 357; Conservative
                                                                                                                 ; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-438-046-1
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09-222-575-13
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LENGTH: 256
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; Sequence 1, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, U1f
; APPLICANT: AASE, Karin
; APPLICANT: DONTN, Annica
; APPLICANT: DONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: OUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: U1f Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; FARLIER FILING DATE: 1999-11-10
; EARLIER FILING DATE: 1998-11-10
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  Score 662; DB 4; 1
Pred. No. 3.9e-164;
0; Mismatches 10;
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ilarity 98.4%;
Conservative
Query Match
Best Local Simila
Matches 679; Co
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09-438-046-1
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IDENTITY_NUC Gapop 10.0 , Scoring table:

32822875 seqs, 18219865908 residues Searched:

Gapext 1.0

65645750 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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gb_est2:*
gb_est3:*
gb_est4:*
gb_est5:*
gb_est6:*
gb_gss1:* EST:* 4 0 M 4 S 9 7 P 8 9 Database

a rinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

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19 100037, P.R. China
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YSVNIREELKLAANVVFFPRCLLVQRCGGGGTVNWRSCTCNSGKTVKKYHEVLQFE
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ä 310 60 TTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGA Gaps 3; Indels Э. Score 1913.2; Pred. No. '0; 0; Mismatches .; 0 98.9%; ilarity 99.7%; Conservative Query Match Best Local Similarity Matches 1928; Conser Ч ò g

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Homo sapiens HCM7077 gene, VI genomic survey sequence.
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AY419997.1 GI:39775954
GSS.

Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1095)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

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Pred. No. 7.5e-218
); Mismatches 1
                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
mol_type="genomic DNA"
db_xref="taxon:9606"
Adams, M.D. and Cargill, M. Inferring nonneutral evolution gene trios Science 302 (5652), 1960-1963
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/locus_tag="HCM7077"
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Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 ' (bases 1 to 1095)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Science 302 (5652), 1960-1963 (2003)
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2 (bases 1 to 1095)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering t
                                                                                                  GAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGGGGGGGTAGAGCTAAGACCATGGCT
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AATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGTTGTGCTGTGTGCTGTGTGGAAATTGTGGCTGTGTAAATGTGGCTGTGCTGCTGCGCTGTGGAGGAAATTGTGGCTGTGCAGCGCTGTGGAGGAAATTGTGGCTGTG
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Pred. No. 1.3e-216
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TRANSCRIPT, partial sequence,
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/protein_id="BAB22735.2"
/brotein_id="BAB22735.2"
/db_xref="G1:26382602"
/db_xref="G1:26382602"
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HLTDLYQREENIQVTSNGHVQSPRFPNSYPRNLLLTWWLRSQEKTRIQLSFDHQFGLE
EAENDICRYDFVEVEVEEVSESSTVVRGRWCGHKEIPPRITTSRTNQIKITFKSDDYFVAK
PGFKIYYSFVEDFQPEAASETNWESVTSSFSGVSYHSPSITDPTLTADALDKTVAEFD
TVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSYHDRKSKVDLDRLNDDVKRYSCTPRN
HSVNLREELKLTNAVFFPRCLLVQRCGGNCGCGTVNWKSCTCSSGKTVKKYHEVLKFE
PGHFKRRGKAKNMALVDIQLDHHERCDCICSSRPPR"
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CCAACCCGCAGCATCAGAGACCAACTGGGAATCTGTCA
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Pred. No. 7.5e-186;
0; Mismatches 311;
                                                                                      db_xref="FANTOM_DB:1110003109'
db_xref="taxon:10090"
clone="1110003109"
                                                                                                                    tissue type="whole body"
clone lib="RIKEN full-length
dev stage="18-day embryo"
86. 1298
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1. .1797
                                                                       mol_type="mRNA"
strain="C57BL/6J"
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llarity 75.5%;
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2 (bases 1 to 1095)
2 (bases 1 to 1095)
3 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

L Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence as made by sequencing genomic exons and ordering the based on alignment.
                                                                                                                                                                       thologous
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Pred. No. 5.7e-166;
0; Mismatches 138;
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Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus'/mol_type="genomic DNA"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 284-304, >AT rich#Low_complexity (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.
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                                                                                    CCAGAGTCATGGCAAGAACATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGGC
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UI-H-DF0-ben-f-24-0-UI.S1 NCI CGAP DF0 Homo sapiens CDNA
UI-H-DF0-ben-f-24-0-UI 3', mRNA sequence.
BU616629
BU616629.1 GI:23282844
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Proj Tumor Gene Index
Unpublished (1997)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-ben-f-24-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
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                 /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.

TAG TISSUE=subchondral bone
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/lab_host="DH10B (Life Technologies)
/clone_lib="NCI_CGAP_DF0"
/note="Organ: Bone; Vector: pT7T3-Pa
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Pred. No. 1.5e-138;
0; Mismatches 3;
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TAG_SEQ=GTTAAGCGTC"
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larity 98.7%;
Conservative
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Eukaryots.

Bukaryots.

Bukaryots.

Bukaryots.

Bukaryots.

Bukaryots.

Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 687)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 284-304, >AT rich#Low_complexity (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers

1. .687

/ organism="Homo sapiens"
/ wol_type="mkNa"
/ db_xref="taxon:9606"
/ clone="UI-H-DF0-ben-p-22-0-UI"
/ tissue_type="Subchondral Bone"
/ dev_stage="Adult"
/ tissue_type="Subchondral Bone"
/ dev_stage="Adult"
/ lab_host="DH10B (Life Technologies)"
/ clone lib="NCI CGAP DF0"
/ note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double strande cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.

TAG TISSUE=subchondral bone
TAG LIB=UI-H-DF0
TAG SEC-GTTAAAGCGTC"
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UI-H-DF0-ben-p-22-0-UI.sl NCI CGAP_DF0 Homo sapiens cDNA clone UI-H-DF0-ben-p-22-0-UI 3', mRNA sequence.
BU616664
BU616664.1 GI:23282879
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Pred. No. 4.2e-136;
0; Mismatches 3;
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illarity 99.5%;
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1 (bases 1 to 606)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of Orthoapedics
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The following repetitive elements were found in this cDNA sequence: 1-24, >AT_rich#Low_complexity 122-142, >AT_rich#Low_complexity 249-325, >(TA)n#Simple_repeat Seq_primer: M13 FORWARD
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            CCAATACCTAAGCATTTTTCCATGAGAAGCACTGCATACTTACCTATGTGGAC
ATAATAGTGTTTGAGGTTATATGCACACACACACACAGAAATATATTCATGT
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BQ575044.1 GI:21478361
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/db_xref="taxon:9606"
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AUTHORS
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/clone="UI-H-EZ1-bbd-o-15-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone lib="NCI CGAP_Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
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TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"
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Pred. No. 4.7e-130;
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//organism="Homo sapiens"
//db_xref="taxon:9606"
/clone="UI-CF-DUI-aav-f-05-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-DUI is a normalized_cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
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Iniversity of Iowa
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University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
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1 (bases 1 to 580)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate discovery
Genome Res. 6 (9), 791-806 (1996)
                                  BU685336
UI-CF-DU1-aav-f-05-0-UI.s2 UI-CF-DU1 Homo sapiens cDNA cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (www.openbiosystems.com).
The following repetitive elements were found in this cDN
sequence: 284-304, >AT_rich#Low_complexity (matched compl
Seq primer: M13 FORWARD
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TAG_LIB=UI-CF-DU1
TAG_SEQ=GGCTGTAGGC"
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Pred. No. 4.1e-113;
0; Mismatches 4;
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McCray Lab
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 799)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9137 row: j column: 14
High quality sequence stop: 664.
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IMAGE:3965677 5',
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601665653F1 NCI_CGAP_Mam1 Mus musculus cDNA clone
mRNA sequence.
BE914552
BE914552.1 GI:10413295
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|clone="IMAGE:3965677"
|tissue_type="tumor, biopsy sample"
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/mol_type="mRNA"
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Mus musculus
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strain="FVB/N"
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam1"
/note="Organ: mammary; Vector: pCMV-SPORT6; SiteSite_2: NotI; Cloned unidirectionally. Primer: Library constructed by Life Technologies. Investproviding samples: Gilbert Smith, NIH"
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Pred. No. 7.6e-113;
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mRNA linear Homo sapiens cDNA,

560 bp resequences, MAGJ

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                         Vertebrata; F
; Hominidae;
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                                                              Gaspard, R., Yeatman,
                                                                                                   in a model
microarray
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     Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebi
Mammalia; Eutheria; Primates; Catarrhini; Homir

(bases 1 to 560)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspi
Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yei
Quackenbush, J.
Assessment of gene expression patterns in a mod
metastasis using a 19,200 element cDNA microari
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, I
Tel: 301 838 3528
Fax: 301 838 6208
Email: johnq@tigr.org
Plate: 258
Seq primer: Forward.
Location/Qualifiers
1. .560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGJ"
/note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                          26.4%; Score 510.8; DB 2;
larity 95.9%; Pred. No. 7.5e-110;
Conservative 0; Mismatches 22;
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AUTHORS
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BU359805
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                                                                                                                     Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                           1 (bases 1 to 508)
Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and Wiemann,S.
EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,Wiemann,S.)
Unpublished (1999)
Contact: MIPS
MIPS
                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.
sequenced by GBF (National Research Centre for Biotechnol
Braunschweig/Germany) within the cDNA sequencing consorti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCCACTCTGATTGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATACAGTC
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                        EST
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                                                                                                                                                                                                                                                                                                                         No sl sequence available.
This clone (DKFZp313A2132) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site
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                        hlcc2) Homo sapiens
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Site_1:
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Pred. No. 4.6e-108;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313A2132"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: h./note="Vector: pTriplEx2; S:cDNA-collection"
                      AL600063

DKFZp313A2132_rl 313 (synonym: h

DKFZp313A2132_5', mRNA sequence.

AL600063

AL600063.1 GI:15163351
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llarity 99.4%;
Conservative
                                                                                             (human)
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Mammalia; Eutheria;
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/lab_nost="DH10B"
/clone lib="CSEQCHN71"
/note="Organ: hearts; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: Not1; This normalized library was
Site_1: EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                  mRNA linear EST 28-NOV-2002 CDNA clone ChEST363b15 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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Galliformes; Phasianidae;
                                   CACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAG
CACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAG
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Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata

Archosauria; Aves; Neognathae; Galliformes; Phasian

Phasianinae; Gallus.

(bases 1 to 819)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burleon, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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Pred. No. 3.3e-107;
); Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST363b15"
/dev_stage="36"
/lab_host="DH10B"
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603477657F1 CSEQCHN71 Gallus gallus
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Department of Biomolecular Sciences
University of Manchester Institute (UMIST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Gallus gallus"
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Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (Mational Institutes of Health, Mammalian Gene Collection (Mutional Institutes of Health, Mammalian Gene Collection (Moublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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  Consortium/LLNL
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Pred. No. 5.4e-105;
0; Mismatches 91;
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           column:
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found through the I.M.A.G.E. http://image.llnl.gov Plate: LLAM11880 row: f co. High quality sequence stop: Location/Qualifiers
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1.505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2695563"
/clone lib="NCI CGAP_Kid11"
/clone lib="NCI CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and 8s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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I (bases 1 to 505)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CG; Tumor Gene Index

Unpublished (1997)

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 475.
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